

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:17 ; Search time 30 Seconds

(Without alignments)
66.644 Million cell updates/secTitle: US-08-854-764-7
Perfect score: 96

Sequence: 1 DSEDEEHTITDTTELPP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802:*

1: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1980 DAT:*

2: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1981 DAT:*

3: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1982 DAT:*

4: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1983 DAT:*

5: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1984 DAT:*

6: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1985 DAT:*

7: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1986 DAT:*

8: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1987 DAT:*

9: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1988 DAT:*

10: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1989 DAT:*

11: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1990 DAT:*

12: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1991 DAT:*

13: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1992 DAT:*

14: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1993 DAT:*

15: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1994 DAT:*

16: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1995 DAT:*

17: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1996 DAT:*

18: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1997 DAT:*

19: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1998 DAT:*

20: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1999 DAT:*

21: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2000 DAT:*

22: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001 DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	96	100.0	18	17	AAR92013	TFPI N-terminal peptide
2	96	100.0	160	13	AAR2800	LAC1 fragment 1
3	96	100.0	161	17	AAR0017	TFPI chimeric protein
4	96	100.0	225	22	AAU02971	Angiotensin convertor
5	96	100.0	256	12	AAR1169	Ser(Asp1-Thr255)-E
6	96	100.0	261	12	AAR1171	Ser-(Asp1-Glu245)-
7	96	100.0	262	12	AAR1172	Ser-(Asp1-Ser248)-
8	96	100.0	265	12	AAR1170	Ser-(Asp1-Ile253)-
9	96	100.0	276	17	AAR9265	TFPI mutant, Lys36
10	96	100.0	276	17	AAR92012	TFPI mutant, K36R.
11	96	100.0	276	18	AAW30311	Recombinant non-g1

OS Synthetic.

PN WO9604377-A1.

XX 15-FEB-1996.

ID AAR92013 standard; Peptide: 18 AA.

XX 25-JUL-1995; 95W0-US09377.

XX 05-AUG-1994; 94US-0286530.

XX (CHIR) CHIRON CORP.

XX Creasey AA, Innis MA;

XX WPI: 1996-129393/13.

Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent

RESULT	PN
AAR1171	W09102753-A.
ID	XX
AAR1171 standard; Protein; 261 AA.	PD
XX	XX
AC	XX
AAR1171;	XX
XX	XX
DT	XX
21-MAY-1991 (first entry)	XX
DE	XX
Se-(Asp1-Glu245)-(Glu262-Met276)-EPI analogue.	DE
XX	XX
KW	XX
Extrinsic pathway inhibitor protein; tissue plasminogen activator;	KW
XX	KW
OS	XX
Synthetic.	OS
XX	XX
PT	XX
W09102753-A.	PT
PN	XX
XX	XX
PD	XX
07-MAR-1991.	PD
XX	XX
PF	XX
17-AUG-1990; 90NO-DK00212.	PF
XX	XX
PR	XX
18-AUG-1989; 89DK-0004080.	PR
XX	XX
DR	XX
WPI; 1991-087248/12.	DR
XX	XX
PF	XX
17-AUG-1990; 90NO-DK00212.	PF
XX	XX
PR	XX
18-AUG-1989; 89DK-0004080.	PR
XX	XX
PA	XX
(NOVO) NOVO NORDISK A/S.	PA
XX	XX
PI	XX
Rasmussen J, Nordfang O;	PI
XX	XX
DR	XX
WPI; 1991-087248/12.	DR
XX	XX
PT	XX
Extrinsic pathway inhibitor protein analogue - useful as	PT
anticoagulant and anti-cancer agent due to low or no	PT
heparin-binding capacity	PT
XX	XX
PS	XX
Claim 5; Page 20; 39PP; English.	PS
XX	XX
CC	CC
Preferred EPI analogues of the invention comprise the first two	Preferred EPI analogues of the invention comprise the first two
CC	CC
kunitz domains of native EPI and have one or more amino acids	kunitz domains of native EPI and have one or more amino acids
CC	CC
deleted in the region Glu148 to the C-terminal Met276, especially	deleted in the region Glu148 to the C-terminal Met276, especially
CC	CC
in the region from Arg245 to Lys275. This analogue is an example of	in the region from Arg245 to Lys275. This analogue is an example of
CC	CC
such a peptide; it has amino acids 249 to 263 of native EPI deleted	such a peptide; it has amino acids 249 to 263 of native EPI deleted
CC	CC
with an optional N-terminal Ser residue. The analogue can be used	with an optional N-terminal Ser residue. The analogue can be used
CC	CC
in a therapeutic composition to treat patients having coagulation	in a therapeutic composition to treat patients having coagulation
CC	CC
disorders or cancer. The analogue has a longer half-life than	disorders or cancer. The analogue has a longer half-life than
CC	CC
full-length EPI. See also AAQ10992-4 and AAR1169-R1170, AAR1172.	full-length EPI. See also AAQ10992-4 and AAR1169-R1170, AAR1172.
XX	XX
Sequence 261 AA;	Sequence 262 AA;
XX	XX
SQ	XX
Query Match 100.0%; Score 96; DB 12; Length 262;	Query Match 100.0%; Score 96; DB 12; Length 262;
Best Local Similarity 100.0%; Pred. No. 7.8e-07; Mismatches 0;	Best Local Similarity 100.0%; Pred. No. 7.8e-07; Mismatches 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;	Matches 18; Conservative 0; Indels 0; Gaps 0;
QV	QV
1 DSDEDEEHTITTELPP 18	1 DSDEDEEHTITTELPP 18
Dv 2 dseedehtittelpp 19	Dv 2 dseedehtittelpp 19
AC	AC
AAR1170;	AAR1170;
XX	XX
AC	AC
AAR1170;	AAR1170;
XX	XX
DT	XX
21-MAY-1991 (first entry)	DT
XX	XX
DE	XX
Se-(Asp1-Tle253)-(Tle266-Met276)-EPI analogue.	DE
XX	XX
KW	XX
Extrinsic pathway inhibitor protein; tissue plasminogen activator;	KW
XX	KW
OS	XX
Synthetic.	OS
XX	XX
PT	XX
W09102753-A.	PT
PN	XX
XX	XX
PD	XX
07-MAR-1991.	PD
XX	XX
PF	XX
17-AUG-1990; 90NO-DK00212.	PF
XX	XX
PR	XX
18-AUG-1989; 89DK-0004080.	PR
XX	XX
PA	XX
(NOVO) NOVO NORDISK A/S.	PA
XX	XX
PI	XX
Rasmussen J, Nordfang O;	PI
XX	XX
DR	XX
WPI; 1991-087248/12.	DR
XX	XX
PT	XX
Extrinsic pathway inhibitor protein analogue - useful as	PT
synthetic.	PT

CC is prep'd. by site-directed mutagenesis of an encoding sequence.

CC In the mutein, the lysine residue in the P1 reactive site of the

CC first Kunitz-type domain of TPPI is replaced by arginine. This

CC domain is required for the inhibition of Factor-VIIa/tissue

CC factor (TF) complex. The mutein may be expressed in *Saccharomyces*

CC cerevisiae transformants, esp. as a ubiquitin fusion protein,

CC and as a Factor-VIIa/TF/Va binding protein.

XX Sequence 276 AA;

Query Match 100.0%; Score 96; DB 17; Length 276;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 18; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 dseeedehtltdtelpp 18

1 dseeedehtltdtelpp 18

RESULT 11

AAW30311 AAW30311 standard; protein; 276 AA.

XX AAW30311;

AC AAW30311;

XX 30-JAN-1998 (first entry)

DE Recombinant non-glycosylated TPPI.

XX Tissue factor pathway inhibitor; TPPI; human; tissue factor inhibitor;

KW lipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI;

KW LACI; extrinsic pathway inhibitor; Protein refolding; clot-inhibitor;

KW protein solubility modification; EPI.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 2 /note= "phosphorylated to varying degrees, but does not

FT affect TPPI function"

FT Disulfide-bond 26..76

FT Disulfide-bond 35..59

FT Disulfide-bond 51..72

FT Disulfide-bond 97..147

FT Disulfide-bond 106..130

FT Disulfide-bond 122..143

FT Disulfide-bond 189..239

FT Disulfide-bond 198..222

FT Disulfide-bond 214..235

XX PN W09640784-A2.

XX DD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09980.

XX PR 07-JUN-1995; 95US-0475668.

XX PA (CHIR) CHIRON CORP.

PA (SEAR) SEARLE & CO. G. D.

XX Arve BH, Bld GS, Chen B, Dorin GJ, Gustafson ME;

PT Hailenbeck RF, Hora MS, Johnson GV, Johnson K, Madani H;

PT Partison GL, Rana RK, Tsang M;

XX DR WPI: 1997-087056/08.

PT Ag formulation of tissue factor pathway inhibitor - contains charged polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation purification and refolding of protein

PS Disclosure; FIG 4; 86pp; English.

CC This sequence represents the human tissue factor pathway inhibitor (TPPI) protein. TPPI is also known as Lipoprotein-associated coagulation inhibitor (LACI), extrinsic pathway inhibitor (EPI) and Tissue factor inhibitor (TFI). The DNA encoding this sequence was altered to contain the optimum codons for expression in *E. coli*, to allow for expression of this protein in the bacteria. TPPI is used in the aqueous formulation of the invention. The aqueous formulation also includes a charged polymer (CP), preferably a sulphated polysaccharide (such as heparin or dextran sulphate) or a polyphosphate, preferably immobilised on a solid support.

CC The CP is added to aid the correct refolding of TPPI. TPPI can also be modified or refolded using the methods of the invention. One method is for modifying the solubility of a protein, by adding an aqueous solution of a CP to reduce inter- and intra-molecular interactions between the charged domains of the protein. The second method is for refolding an improperly folded or denatured protein (e.g. TPPI), and comprises adding CP to a solution of the protein prior to allowing the protein to refold.

CC The methods are particularly useful for solubilising, formulating, purifying and refolding proteins (especially TPPI) which have been engineered by genetic recombination and produced in bacterial, yeast or other cells in a form that has a non-native tertiary structure. TPPI is a

CC coagulation inhibitor which has clot-inhibiting properties.

XX Sequence 276 AA;

Query Match 100.0%; Score 96; DB 18; Length 276;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 18; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 dseeedehtltdtelpp 18

1 dseeedehtltdtelpp 18

RESULT 12

AAW61535 AAW61535 standard; protein; 276 AA.

XX AC AAW61535;

XX DT 06-NOV-1998 (first entry)

DE Human tissue factor pathway inhibitor (TPPI).

XX KW Human tissue factor pathway inhibitor; TPPI; TPPI-2; cell proliferation;

KW angiogenesis related disease; cancer; arthritis; macular degeneration;

KW diabetic retinopathy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 2 /note= "Potential phosphorylation site"

FT Domain 26..76 /note= "Kunitz-1 type protease inhibitor domain"

FT Disulfide-bond 26..76

FT Disulfide-bond 35..59

FT Disulfide-bond 51..72

FT Disulfide-bond 97..147

FT Disulfide-bond 106..130

FT Disulfide-bond 117

FT Disulfide-bond 122..143

FT Disulfide-bond 167

FT Modified-site /note= "N-glycosylated"

FT Domain 189..239 /note= "Kunitz-3 type protease inhibitor domain"

FT Disulfide-bond 198..222

FT Region /note- "Potential N-linked glycosylation site"
 FT Region 31..53 /note- "See comments below"
 FT Region 82..88 /note- "See comments below"
 FT Region 153..156 /note- "See comments below"
 FT Region 153..156 /note- "See comments below"
 XX
 PN EP018451-A.
 XX
 PD 31-MAY-1989.
 XX
 PF 22-JUL-1988; 88EP-0870127.
 XX
 PR 23-NOV-1987; 87US-013753.
 XX
 PA (MONS) MONSANTO CO (UNIW).
 XX
 Broze GJ, Kretzmer KK, Wun TC;
 PR WPI; 1989-150483/22.
 DR N-PSDB; AAN90108.
 XX
 PT DNA encoding human tissue factor inhibitor
 - used in study of coagulation cascade for agents
 which inhibit factor Xa and Factor VIIa-TF
 XX
 PS Claim 3; Figure 3; 14pp; English.
 XX
 Amino acid sequence of tissue factor inhibitor (TFI) cDNA isolate from
 lambda-39 clone of human placenta cDNA library. Domains discerned
 include: highly negatively charged N-terminal; highly positively charged
 carboxy terminus; intervening portion consisting of 3 homologous domains
 with sequences typical of Kunitz-type enzyme inhibitors. Based on
 homology study, it appears to be a member of the basic protease
 inhibitor gene superfamily. Sequences in misc. regions in feature table
 above have been independently confirmed by amino acid sequence analysis.
 XX
 SQ Sequence 304 AA;

FT Region /note- "Kunitz domain LACI-K3"
 XX
 PN WO9521601-A2.
 XX
 PD 17-AUG-1995.
 XX
 PR 11-JAN-1995; 95WO-US00299.
 XX
 PR 10-MAR-1994; 94US-0208264.
 XX
 PR 11-JAN-1994; 94US-0179364.
 XX
 PA (PROT-) PROTEIN ENG CORP.
 XX
 PI Ladher RC, Markland W;
 XX
 WPI; 1995-292934/38.
 XX
 PT Kallikrein inhibiting proteins comprising a Kunitz domain homologous
 to bovine pancreatic trypsin inhibitor - useful for preventing or
 treating disorders attributable to excessive kallikrein activity,
 e.g. in hereditary angioedema.
 XX
 DR Disclosure; Page 24; 46pp; English.
 XX
 CC AAR81884 is the human lipoprotein-associated coagulation inhibitor
 which is a Kallikrein
 LACI. The Kunitz domain, LACI-K1, of LACI is a Kallikrein
 inhibiting protein (KIP) upon which the claimed KIPs of the invention
 are based. The KIPs can be used for treating or preventing disorders
 attributable to excessive kallikrein activity, e.g. hereditary
 angioedema. The KIPs can also be used for assaying, purifying and in
 vivo imaging of kallikrein.
 XX
 SQ Sequence 304 AA;

Query Match 100.0%; Score 96; DB 16; Length 304;
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEEDDEEHTLITDTELPP 18
 ||||| ||||| ||||| |||||
 Db 29 dseeddeehhtlitttelpp 46

Search completed: September 20, 2002, 10:28:38
 Job time: 81 sec

RESULT 15
 AAR81884
 ID AAR81884, standard: protein; 304 AA.
 XX
 AC AAR81884;
 XX
 DT 18-MAR-1996 (first entry)
 DE Lipoprotein-associated coagulation inhibitor (LACI).
 XX
 KW Lipoprotein-associated coagulation inhibitor; LACI; kallikrein;
 KW inhibitor; KIP; Kunitz domain; hereditary angioedema.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FT Peptide 1..28
 FT /label= sig_peptide
 FT Domain 50..107
 FT /note- "Kunitz domain LACI-K1"
 FT Domain 121..178
 FT /note- "Kunitz domain LACI-K2"
 FT Domain 213..270

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

ON protein - protein search, using sw model

Run on:

September 20, 2002, 10:27:17 ; Search time 12.96 Seconds

(without alignments)

33.924 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96

Sequence: 1

DSEDEEHTITDBTELP

18

Scoring table: BLOSUM62

Gapop 1.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : issued_patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMBO.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMBO.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMBO.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMBO.pep:*

5: /cgn2_6/ptodata/2/1aa/PCPTUS_COMBO.pep:*

6:- /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC compatible	SOFTWARE: PatentIn Release #1.0, Version #1.30B	CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08854764	CLASSIFICATION: 435	PRIOR APPLICATION DATA:	APPLICATION NUMBER: 08/286,530	FILED: 05-AUG-1994	ATTORNEY/AGENT INFORMATION:	NAME: Saverinde, Paul B.	REGISTRATION NUMBER: 36,914	REFERENCE/DOCKET NUMBER: 0991.001	TELECOMMUNICATION INFORMATION:	TELEPHONE: 510-601-2285	TELEFAX: 510-625-3512	INFORMATION FOR SEQ ID NO: 7:	SEQUENCE CHARACTERISTICS:	LENGTH: 18 amino acids	TYPE: amino acid	STRANDEDNESS: single	TOPOLOGY: linear	MOLECULE TYPE: peptide	US-08-854-764-7
1	96	100.0	18	3: US-08-854-764-7	Sequence 7, Appli																								
2	96	100.0	18	5: PCT-US95-09377-7	Sequence 7, Appli																								
3	96	100.0	161	1: US-08-437-841-19	Sequence 7, Appli																								
4	96	100.0	161	1: US-08-437-841-19	Sequence 7, Appli																								
5	96	100.0	161	1: US-08-437-841-19	Sequence 7, Appli																								
6	96	100.0	161	4: US-08-943-682-19	Sequence 7, Appli																								
7	96	100.0	161	5: PCT-US95-09464-19	Sequence 7, Appli																								
8	96	100.0	189	1: US-07-829-920A-7	Sequence 7, Appli																								
9	96	100.0	189	1: US-07-829-920A-1	Sequence 7, Appli																								
10	96	100.0	276	1: US-08-437-841-9	Sequence 9, Appli																								
11	96	100.0	276	1: US-08-286-521-9	Sequence 9, Appli																								
12	96	100.0	276	1: US-08-436-175-9	Sequence 9, Appli																								
13	96	100.0	276	2: US-08-796-850-1	Sequence 9, Appli																								
14	96	100.0	276	3: US-08-854-764-3	Sequence 9, Appli																								
15	96	100.0	276	4: US-08-943-682-9	Sequence 9, Appli																								
16	96	100.0	276	5: PCT-US95-09377-3	Sequence 9, Appli																								
17	96	100.0	276	5: PCT-US95-09464-9	Sequence 9, Appli																								
18	96	100.0	277	1: US-07-844-297-1	Sequence 9, Appli																								
19	96	100.0	304	1: US-08-024-145-2	Sequence 9, Appli																								
20	96	100.0	304	1: US-08-446-646-9	Sequence 9, Appli																								
21	96	100.0	304	1: US-08-943-682-9	Sequence 9, Appli																								
22	96	100.0	304	2: US-09-130-012A-18	Sequence 18, Appli																								
23	96	100.0	304	3: US-08-676-124-1	Sequence 1, Appli																								
24	96	100.0	304	3: US-08-208-264A-25	Sequence 1, Appli																								
25	96	100.0	304	3: US-09-411-878-1	Sequence 1, Appli																								
26	96	100.0	304	3: US-09-240-136-1	Sequence 1, Appli																								
27	96	100.0	304	4: US-09-054-782-2	Sequence 2, Appli																								

Query Match 100.0%; Score 96; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.1e-08; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSFEDDEHTTITTELPP 18
Db 1 1111111111111111
Qy 1 DSFEDDEHTTITTELPP 18

RESULT 2
PCT-US95-09377-7

SEQUENCE 7, Application PC/TUSS9509377

GENERAL INFORMATION

APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Production of Tissue Factor Pathway
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT-US95/09377
FILING DATE: 25-JULY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saveridge, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542

SEQUENCE FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

PCT-US95-09377-7

Query Match Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-08-286-521-19

SEQUENCE 19, Application US/08286521

GENERAL INFORMATION

APPLICANT: Innis, Michael
APPLICANT: Creasy, Aba
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286.521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Saveridge, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542

SEQUENCE FOR SEQ ID NO: 19:

LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single

RESULT 3
US-08-437-841-19

SEQUENCE 19, Application US/08437841

GENERAL INFORMATION

APPLICANT: Innis, Michael
APPLICANT: Creasy, Aba
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

TOPOLGY: linear
 MOLECULE TYPE: peptide
 US-08-286-521-18
 Query Match. 100.0%; Score 96; DB 1; Length 161;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DSEDEDEHTITDTELPP 18
 Db 1 DSEDEDEHTITDTELPP 18

RESULT 5
 US-08-436-175-19
 Sequence 19, Application US/08436175
 Patent No. 5636088
 GENERAL INFORMATION:
 APPLICANT: Innis, Michael
 APPLICANT: Creasey, Abla
 TITLE OF INVENTION: Chimeric Proteins
 NUMBER OF SEQUENCES: 37
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943.682
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/438.184
 FILING DATE: 09-MAY-1995
 APPLICATION NUMBER: US 08/286.521
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveriote, Paul B.
 REGISTRATION NUMBER: 36.914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3342
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLGY: linear
 MOLECULE TYPE: peptide
 US-08-943-682-19

Query Match. 100.0%; Score 96; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DSEDEDEHTITDTELPP 18
 Db 1 DSEDEDEHTITDTELPP 18

RESULT 7
 PC-US95-0964-19
 Sequence 19, Application PC/US9509464
 GENERAL INFORMATION:
 APPLICANT: CHIRON CORPORATION
 TITLE OF INVENTION: Chimeric Proteins
 NUMBER OF SEQUENCES: 37
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PC/US95/09464
 FILING DATE: 25-JULY-1995

RESULT 6
 US-08-943-682-19
 Sequence 19, Application US/08943682
 Patent No. 6174721
 GENERAL INFORMATION:

CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
NAME: Sanderle, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
ID-US5-09601-19

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sawyeride, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990-100
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ID: PT-US95-09460-19

Query Match 100.0%; Score 96; DB 1; Length 189;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSDEDEHTTITDTELPP 18
 Db 29 DSDEDEHTTITDTELPP 4.6

RESULT 9
 US-07-828-920A-1
 Sequence 1, Application US/07828920A
 Patent No. 5312736
 GENERAL INFORMATION:
 APPLICANT: Rasmussen, Jesper
 NO. 5312736djang, Ole Juul
 TITLE OF INVENTION: Anticoagulant Protein
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5312736djang, Ole Juul
 STREET: 405 Lexington Avenue, Suite 6200
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/828, 920A
 FILING DATE: 19920127
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 4080/89
 FILING DATE: 18-AUG-1989
 APPLICATION NUMBER: WO PCT/DK90/00212
 FILING DATE: (17)AUG1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Zelson, Steve T.
 REGISTRATION NUMBER: 30335
 REFERENCE/DOCKET NUMBER: 3287.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1.276
 US-07-828-920A-1

Query Match 100.0%; Score 96; DB 1; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSDEDEHTTITDTELPP 18
 Db 1 DSDEDEHTTITDTELPP 18

RESULT 10
 US-07-828-920A-1

US-08-437-841-9
; Sequence 9, Application US/08437841

PATENT NO. 5563123
 GENERAL INFORMATION:
 APPLICANT: Innis, Michael
 APPLICANT: Creasey, Abla
 TITLE OF INVENTION: Chimeric Proteins
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,521
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveride, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEXFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-286-521-9

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/37,841
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,521
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveride, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEXFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-437-841-9

Query Match 100 %; Score 96; DB 1; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEEDBEHTITDTELP 18
 Db 1 DSEEDBEHTITDTELP 18

RESULT 122
 US-08-436-175-9
 Sequence 9, Application US/08436175
 PATENT NO: 5596088
 GENERAL INFORMATION:
 APPLICANT: Innis, Michael
 APPLICANT: Creasey, Abla
 TITLE OF INVENTION: Chimeric Proteins
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,175
 FILING DATE: 09-MAY-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,521
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveride, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEXFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-436-175-9

RESULT 11
 US-08-286-521-9
 Sequence 9, Application US/08286521
 PATENT NO: 5589359
 GENERAL INFORMATION:
 APPLICANT: Innis, Michael
 APPLICANT: Creasey, Abla
 TITLE OF INVENTION: Chimeric Proteins
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,175
 FILING DATE: 09-MAY-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,521
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveride, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEXFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-436-175-9

Query Match Simularity 100.0%; Score 96; DB 1; Length 276;
 Best Local Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEEDBEHTTIDTELP 18
 Patent No. 5981471
 Db 1 DSEEDBEHTTIDTELP 18

RESULT 13
 APPLICANT: Papathanassiu, Adonia E
 APPLICANT: Green, Shawn J.
 TITLE OF INVENTION: Compositions and Methods for Inhibiting
 NUMBER OF SEQUENCES: 2
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.A.
 ZIP: 30303
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/796,850
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Greene, Jamie L.
 REGISTRATION NUMBER: 32,467
 REFERENCE/DOCKET NUMBER: 05213-0290
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-2700
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE: Homo sapiens
 ORGANISM: Homo sapiens
 FEATURE: Active-site
 NAME/KEY: Active-site
 LOCATION: 2..3
 OTHER INFORMATION: /note- "Site of partial
 glycosylation"

OTHER INFORMATION: /note- "Potential site for N-linked glycosylation."
 OTHER INFORMATION:
 NAME/KEY: Domain
 LOCATION: 26..76
 OTHER INFORMATION: /label- Kunitz-1
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 97..147
 OTHER INFORMATION: /label- Kunitz-2
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 189..239
 OTHER INFORMATION: /label- Kunitz-3
 US-08-796-850-1

Query Match Simularity 100.0%; Score 96; DB 2; Length 276;
 Best Local Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEEDBEHTTIDTELP 18
 Db 1 DSEEDBEHTTIDTELP 18

RESULT 14
 US-08-854-764-3
 Sequence 3, Application US/08854764
 Patent No. 6103500
 GENERAL INFORMATION:
 APPLICANT: Innes, Michael
 APPLICANT: Creasey, Abigail
 TITLE OF INVENTION: Production of Tissue Factor Pathway Inhibitor
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,764
 FILING DATE: 12-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/286,530
 FILING DATE: 05-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saverende, Paul B.
 REGISTRATION NUMBER: 36,914
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match Simularity 100.0%; Score 96; DB 3; Length 276;

Best local similarity 100.0%; Pred. No. 4.1e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 18;

QY 1 DSEDEEHTITDTELPP 18
Db 1 DSEDEEHTITDTELPP 18

RESULT 15

US-08-943-682-9

Sequence 9, Application US/08943682

GENERAL INFORMATION:

Patent No. 6174721

APPLICANT: Tonis, Michael
TITLE OF INVENTION: Chimeric Proteins

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,682

FILING DATE: 03-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/438,184

FILING DATE: 09-MAY-1995

APPLICATION NUMBER: US 08/286,521

FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Savereide, Paul B.

REGISTRATION NUMBER: 36,914

REFERENCE/DOCKET NUMBER: 0990.001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-601-2585

TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-943-682-9

Query Match 100.0%; Score 96; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTELPP 18
Db 1 DSEDEEHTITDTELPP 18

Search completed: September 20, 2002, 10:27:39
Job time: 22 sec

GenCore version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

ON Protein - protein search, using SW model

Run on: September 20, 2002, 10:27:17 ; Search time 14.76 seconds

(without alignments) 117.182 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96

Sequence: 1 DSEDEDEHTITDTELPP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71;*

1: Pirl;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1

TIHCK tissue factor pathway inhibitor precursor [validated] - human

N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000

C;Accession: A23712; A39176; A26650; A60433; B60433; S13054; A34315; A38294; S03903

R;Giard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M

J;Biol. Chem. 266, 5036-5041, 1991

J;Biol. Chem. 266, 5036-5041, 1991

A;Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. In

A;Reference number: A23712; MUID:9161593

A;Accession: A23712

A;Molecule type: DNA

A;Residues: 1-304 <GIR>

A;Cross-references: GB:MB59493; GB:MB59499; NID:9187204; PIDN:AAA59526; 1; PID:9187205

R;van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.

Biochemistry 30, 1571-1577, 1991

A;Title: Intron-exon organization of the human gene coding for the lipoprotein-associ

A;Reference number: A39176; MUID:9129227

A;Accession: A39176

A;Molecule type: DNA

A;Residues: 1-304 <VAN>

A;Cross-references: GB:MB56550; GB:J05312; NID:9186827; PIDN:AAA59480; 1; PID:9186829.

R;Wun, T.C.; Kretzmer, G.K.; Giard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J;Biol. Chem. 263, 6001-6004, 1988

A;Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated

A;Reference number: A28650; MUID:88198127

A;Accession: A28650

A;Molecule type: mRNA

A;Residues: 1-125 <WIND>

A;Cross-references: GB:J03225; NID:9180545; PIDN:AAA52022; 1; PID:9180546

A;Note: part of this sequence, including the amino end of the mature protein, was con

R;Giard, T.J.; Warren, L.D.; Novotny, W.F.; Beleck, B.E.; Miletich, J.P.; Broze Jr.,

Thromb. Res. 55, 37-50, 1989

A;Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associa

A;Reference number: A60433; MUID:89388722

A;Accession: A60433

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-304 <G12>

A;Experimental source: endothelial cells

A;Accession: B60433

A;Molecule type: protein

A;Residues: XX, 3153, X, 55-56 <G13>

A;Experimental source: recombinant material from mouse C137 cells

R;Giard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr.,

Biochem. J. 270, 621-625, 1990

A;Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibit

A;Reference number: S13034; MUID:91054349

A;Accession: S13034

A;Molecule type: protein

A;Residues: 29-35 <G14>

30 44 45.8 1401 2 T48079 hypothetical prote

31 44 45.8 2175 1 S03170 homeotic protein c

32 43.5 45.3 552 2 T27427 hypothetical prote

33 43.5 45.3 1188 2 JC8889 phosphatidylinosit

34 43 44.8 239 2 S62527 phospholipase C (E

35 43 44.8 449 2 D69037 PEP12-like prote

36 43 44.8 489 2 A31555 interferon gamma r

37 43 44.8 515 2 A42289 CD41 Protein - hu

38 43 44.8 699 2 S25541 heat shock protein

39 43 44.8 1038 1 JC557 DNA-directed DNA P

40 43 44.8 1038 2 T18222 DNA polymerase del

41 43 44.8 1054 2 T39901 cyclic nucleotide

42 43 44.8 1105 1 S4043 DNA-directed DNA P

43 43 44.8 1106 1 A32299 DNA-directed DNA P

44 43 44.8 1107 1 A41610 phospholipase C-be

45 43 44.8 1217 2 A45493

ALIGNMENTS

R; Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 264, 18832-18837, 1989
 A; Reference number: A34315; MUID:9036996
 A; Accession: A34315
 A; Molecule type: protein
 A; Residues: 'XX', 31-33, 'L', 35-50 <NOV>
 A; Experimental source: plasma
 R; Pedersen, A.H.; Norgaard, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.; J. Biol. Chem. 265, 16786-16793, 1990
 A; Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and characterization of the lipoprotein-associated coagulation inhibitor
 A; Reference number: A38294; MUID:91009092
 A; Molecule type: protein
 A; Residues: 245-41 <PEP>
 R; Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; Nature 338, 518-520, 1989
 A; Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-ase
 A; Reference number: S03903; MUID:89181950
 A; Contents: annotation; site-directed mutagenesis
 C; Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the second domain binds factor Xa/tissue factor complex
 C; Genetics:
 A; Gene: GDB:TFPI
 A; Cross-references: GDB:127364; OMIM:152310
 A; Map position: 2q32-2q32
 A; Introns: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
 C; Function:
 A; Description: regulates clotting by factor Xa-dependent inhibition of the coagulation factor VIIa/tissue factor complex
 C; Species: *Saccharomyces cerevisiae*
 C; Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding protein; heparin binding protein; heparin binding protein; inhibitor; inhibitor homology
 F; 1-28/Domain: signal sequence <SIG>
 F; 2-9/304/Domain: tissue factor pathway inhibitor homology <SIG>
 F; 54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F; 217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F; 284-289/Region: heparin binding <SIG>
 F; 3/30/Bindin: site: phosphatidylserine <SIG>
 F; 54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #
 F; 64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
 F; 135/Inhibitory site: Lys (coagulation factor X) #status predicted
 F; 145, 195, 256/Binding site: Arg (coagulation factor Xa) #status predicted
 F; 227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match Score 96; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTTITDTELPP 18
 Db 29 DSEDEEHTTITDTELPP 46

RESULT 2

JC2264 tissue factor pathway inhibitor precursor - rhesus macaque
 N; Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibitor
 C; Species: *Macaca mulatta* (rhesus macaque)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C; Accession: JC2264
 R; Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamoto, J.; Biochem. 115, 708-714, 1994
 A; Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
 A; Reference number: JC2264; MUID:94375417
 A; Accession: JC2264
 A; Molecule type: mRNA
 A; Residues: 1-304 <KAN>
 A; Cross-references: GB:573337; NID:q685016; PIDN:AAB31955.1; PID:q685017
 A; Experimental source: liver
 C; Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VII
 C; Keywords: anticoagulant; tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

Query Match Score 96; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTTITDTELPP 18
 Db 29 DSEDEEHTTITDTELPP 46

RESULT 3

S56221 hypothetical protein YFL033c - yeast (*Saccharomyces cerevisiae*)
 C; Species: *Saccharomyces cerevisiae*
 C; Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 29-Oct-1999
 C; Accession: S56221
 R; Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas submitted to the EMBL Data Library, May 1995
 A; Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*
 A; Reference number: S56186
 A; Accession: S56221
 A; Molecule type: DNA
 A; Residues: 1-1770 <UR>
 A; Cross-references: EMBL:DS0617; NID:9836685; PIDN:BA009206.1; PID:ds0617; PID:9836685
 C; Genetics:
 A; Gene: SGD:RIM15
 A; Cross-references: SGD:S0001861; MIPs:YFL033C
 A; Map position: 6L

Query Match Score 96; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTTITDTELPP 18
 Db 29 DSEDEEHTTITDTELPP 46

RESULT 4

T26063 hypothetical protein W01F3.3 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C; Accession: T26063
 R; Cummings, P.; submitted to the EMBL Data Library, March 1997
 A; Reference number: Z20145
 A; Accession: T26063
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-2225 <WIL>
 A; Cross-references: EMBL:292815; PIDN:CA07294.1; GSPDB:GN00023; CESP:W01F3.3
 A; Experimental source: clone W01F3
 C; Genetics:
 A; Gene: CESP:W01F3.3
 A; Map position: 5
 A; Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221

Query Match Score 55; DB 2; Length 2225;

Best Local Similarity 55.6%; Pred. No. 6.7%; Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTITDTELP 18
Db 663 DTEEDDEHAWPITTP 680

RESULT 5

JC4833 homeobox protein zhx-1 - mouse
N:Alternative names: homeobox-containing protein zhx-1
C:Species: *Mus musculus* (house mouse)
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jul-2000
C;Accession: JC4863
R;Barthelmy, I.; Carramolino, L.; Gutierrez, J.; Barbero, J.L.; Marquez, G.; Zaballos, Biochem. Biophys. Res. Commun. 224, 870-876, 1996
A;Title: zhx-1: A novel mouse homeodomain protein containing two zinc-fingers and five
A;Reference number: JC4863; MUID:96311380
A;Contents: bone
A;Accession: JC4863
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-873
A;Cross-references: EMBL:254200; NID:92687851; PIDN:CAA9005.1; PID:91504088
C;Comment: This protein belongs to zinc-finger class of homeodomain transcription factor
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: bone; DNA binding; homeobox; nucleus; transcription regulation; zinc finger
F;70-93/Region: zinc finger
F;102-125/Region: zinc finger
F;285-341/Domain: homeobox homology <HOX1>
F;465-521/Domain: homeobox homology <HOX2>
F;561-625/Domain: homeobox homology <HOX3>
F;661-717/Domain: homeobox homology <HOX4>
F;741-765/Region: arginine/glycine-rich
F;771-827/Domain: homeobox homology <HOX5>

Best Local Similarity 53.1%; Score 51; DB 2; Length 873; Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTITDTELP 18
Db 844 DQEEDDEETDDSDTW 861

RESULT 6

JC7079 homeobox protein ZHXL - human
C:Species: *Homo sapiens* (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7079
R;Yamada, K.; Printz, R.L.; Osawa, H.; Granner, D.K., Biochem. Biophys. Res. Commun. 261, 614-621, 1999
A;Title: Human ZHXL: Cloning, chromosomal location, and interaction with transcription factors
A;Reference number: JC7079; MUID:9373128
A;Accession: JC7079
A;Molecule type: mRNA
A;Residues: 1-873
A;Cross-references: GB:AF0106862; NID:95757883; PIDN:RAD50624.1; PID:95757884
A;Experimental source: liver
A;Gene: zhl
A;Map position: 8q
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: bone; DNA binding; homeobox; nucleus; transcription regulation; zinc finger
F;70-93/Region: zinc finger
F;102-125/Region: zinc finger
F;285-341/Domain: homeobox homology <HOX1>
F;465-521/Domain: homeobox homology <HOX2>
F;561-625/Domain: homeobox homology <HOX3>
F;661-717/Domain: homeobox homology <HOX4>

Best Local Similarity 53.1%; Score 51; DB 2; Length 873; Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTITDTELP 18
Db 844 DQEEDDEETDDSDTW 861

RESULT 7

JE0209 brain specific angiogenesis inhibitor-associated protein 1 - human
C:Alternate names: BAI1-associated protein 1; BAI1 [misnomer]
C;Species: *Homo sapiens* (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 18-Aug-2000
C;Accession: JE0209
R;Shirasuchi, T.; Futamura, M.; Oda, K.; Nishimori, H.; Nakamura, Y.; Tokino, T., Biochem. Biophys. Res. Commun. 247, 597-604, 1998
A;Title: Cloning and characterization of BAI-associated protein 1: A PDZ domain-containing protein
A;Reference number: J50209; MUID:98321173
A;Accession: JE0209
A;Molecule type: mRNA
A;Residues: 1-1256 <SH1>
A;Cross-references: GB:AB010894; NID:93370997
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAIAP1; BAI1
A;Cross-references: GDB:9864783
A;Map position: 3P14.1-3P14.1
C;Superfamily: WW repeat homology
C;Genetics:
A;Gene: GDB:BAIAP1; BAI1
A;Cross-references: GDB:9864783
A;Map position: 3P14.1-3P14.1
C;Superfamily: WW repeat homology <WW1>
F;300-337/Domain: WW repeat homology <WW2>
F;359-396/Domain: WW repeat homology <WW2>

Best Local Similarity 52.6%; Score 50.5; DB 2; Length 1256; Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 DSEDEDEHTITDTELP 18
Db 254 DSQEDEHT-LOETALPP 270

RESULT 8

A4037 glutamic acid-rich protein, retinal - bovine
C;Species: Bos Primigenius taurus (cattle)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C;Accession: A4037
R;Sugimoto, Y.; Yatsuhashi, K.; Tsujimoto, M.; Khorana, H.G.; Ichikawa, A., Proc. Natl. Acad. Sci. U.S.A. 88, 3116-3119, 1991
A;Title: The amino acid sequence of a glutamic acid-rich protein from bovine retina
A;Reference number: A4037; MUID:91195303
A;Accession: A4037
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <SUG>
A;Cross-references: GB:M61185; NID:9163077; PIDN:AAA30536.1; PID:9163078

Best Local Similarity 51.0%; Score 49; DB 2; Length 590; Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTITDTELP 18
Db 459 DQEEDQHDSVLDSYLV 476

RESULT 9
 S55352 IFH1 protein - [Yeast \(Saccharomyces cerevisiae\)](#)
 N:Alternate name: protein L8083; 9; protein YLR223c; RRP3 protein
 C;Species: *Saccharomyces cerevisiae*
 C;Accession: S55352; S51446; S47477
 R;Cherel, I.; Thuriaux, P.
 A;Title: The IFH1 gene product interacts with a fork head protein in *Saccharomyces cerevisiae*
 A;Reference number: S55352; MUID:9530839
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Accession: 14985 <CHB>
 A;Cross-references: EMBL:Z29488; NID:9531491; PIDN:CAA82624.1; PID:g531492
 R;Hallsworth, K.
 A;Submitted to the EMBL Data Library, December 1994
 A;Description: The sequence of *S. cerevisiae* cosmid 8083.
 A;Reference number: S51443
 A;Accession: S51446
 A;Molecule type: DNA
 A;Residues: 1-1085 <HAL>
 A;Cross-references: EMBL:U19027; NID:9609363; PID:g609372; MIPS:YLR223c
 C;Genetics:
 A;Gene: SGD:IFH1; RRP3
 A;Cross-references: SGD:S0004213; MIPS:YLR223c
 A;Map position: 12R

Query Match, Similarity 50.0%; Score 48; DB: 2; Length 1085;
 Best Local Similarity 47.1%; Pred. No. 35; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSEDEEHTITDTELP 17
 Db 404 DEEDDEEDEIMSDEDMP 420

RESULT 10
 A49457 fibulin-2 precursor - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 11-Jan-2000
 R;Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
 J. Cell Biol. 123, 1299-1277, 1993
 A;Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with
 A;Reference number: A49457; MUID:94064787
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1221 <PAN>
 A;Cross-references: GB:Y75285; NID:g437046; PIDN:CAA3040.1; PID:g437047
 R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 240, 427-434, 1996
 A;Title: Different susceptibility of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases
 A;Reference number: S74094; MUID:96439073
 A;Molecule type: protein
 A;Residues: 236-238, X, 240-247, 260-275, 336-344, 'L', 346-361; 405-426, 566-568, 'EM', 569-589
 C;Superfamily: unassigned EGF-related proteins; EGF homology
 C;Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
 F;942-978/Domain: EGF homology <EGF>

Query Match, Similarity 49.5%; Score 47; DB: 2; Length 1221;
 Best Local Similarity 50.0%; Pred. No. 48; Mismatches 4; Indels 3; Gaps 1;
 Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

Qy 1 DSEDEEHTITDTELP 18
 Db 274 DEEEEEEETIVTE---PP 288

RESULT 11
 S12143 lipoprotein-associated coagulation inhibitor precursor - rabbit
 N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue ze
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C;Accession: S12143; A61373
 R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
 Nucleic Acids Res. 18, 6440, 1990
 A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor
 A;Reference number: S12143; MUID:91051146
 A;Accession: S12143
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-300 <WES>
 A;Cross-references: EMBL:X54708; NID:91612; PIDN:CAA38515.1; PID:g1613
 R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
 J. Cell. Physiol. 148, 320-326, 1991
 A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial
 A;Reference number: A61373; MUID:91349227
 A;Accession: A61373
 A;Molecule type: protein
 A;Residues: 25-33, 'X', 35-46 <COL>
 C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 C;Keywords: anticoagulant; glycoprotein
 F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 Query Match, Similarity 49.0%; Score 47; DB: 2; Length 300;
 Best Local Similarity 42.5%; Pred. No. 11; Mismatches 4; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SEEDEEHTITDTELP 17
 Db 26 AEEDEEHTNITDIKPP 41

RESULT 12
 S69063 probable membrane protein YPR075c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein P0513.9
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Feb-1998
 C;Accession: S69063
 R;Couch, J.
 submitted to the EMBL Data Library, March 1996
 A;Description: The sequence of *S. cerevisiae* cosmid 9513.
 A;Reference number: S69057
 A;Accession: S69063
 A;Molecule type: DNA
 A;Residues: 1-360 <COL>
 A;Cross-references: EMBL:U51033; NID:91230676; PID:g1230683; MIPS:YPR075c
 C;Genetics:
 A;Gene: SGD:OPY2
 A;Cross-references: SGD:S0006279; MIPS:YPR075c
 A;Map position: 16R
 C;Keywords: transmembrane protein
 F;96-112/Domain: transmembrane protein

Query Match, Similarity 49.0%; Score 47; DB: 2; Length 360;
 Best Local Similarity 47.1%; Pred. No. 13; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSEDEEHTITDTELP 17
 Db 318 DEDDDEEGSFIDLEIP 334

RESULT 13
 AD1209 N-acetyl muramoyl-L-alanine amidase (EC 3.5.1.28) lmo1076 - Listeria monocytogenes (strain C; Species: *Listeria monocytogenes* C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2001 C; Accession: AD1209 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 264, 849-852, 2001 A; Authors: Kretft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Mok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of *Listeria* species A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-572 <GLA> A; Cross-references: GB:NC_003210; PIDN: CAC99154.1; PID: g16410478; GSPDB: GN00177 A; Experimental source: strain EGD-e A; Genetics: C; Gene: lmo1076 A; Keywords: hydrolase

RESULT 14
 A46719 inositol 1,4,5-trisphosphate receptor subtype 3 - rat C; Species: *Rattus norvegicus* (Norway rat) C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999 C; Accession: A46719 R; Blondel, O.; Takeda, J.; Janssen, H.; Seino, S.; Bell, G.I. J. Biol. Chem. 268, 11356-11363, 1993 A; Title: Sequence and functional characterization of a third inositol trisphosphate receptor A; Reference number: A46719; MUID: 93266594 A; Accession: A46719 A; Status: preliminary A; Molecule type: nucleic acid A; Residues: 1-2670 <BLO> A; Cross-references: GB:L06096; NID: g310170; PIDN: AAM41446.1; PID: g310171 A; Experimental source: insulinoma cell line RINm5F A; Note: sequence extracted from NCBI backbone (NCBIN:132840, NCBIP:132841) C; Superfamily: inositol-trisphosphate receptor

Query Match 47.9%; Score 46; DB 2; Length 572; Best Local Similarity 44.4%; Pred. No. 33; Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0; Job time: 45 sec

Qy 1 DSEDEDEHTITDTELP 18
 Db 34 DSSEQDNTTEVAREMPP 51

RESULT 15
 T20784 hypothetical protein F1D11.7 - *Caenorhabditis elegans* C; Species: *Caenorhabditis elegans* C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T20784 R; Mortimore, B.; Basham, V. submitted to the EMBL Data Library, November 1996 A; Reference number: 219323 A; Accession: T20784

Query Match 46.9%; Score 45; DB 2; Length 244; Best Local Similarity 47.1%; Pred. No. 17; Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0; Job time: 45 sec

Qy 1 DSEDEDEHTITDTELP 17
 Db 78 ESDRSEPHVAKTELP 94

A; Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA

A; Residues: 1-244 <WIL>

A; Cross-references: EMBL:281500; PIDN: CAB04102.1; GSPDB: GN00023; CESP:F1D11.7

A; Experimental source: clone F1D11

C; Genetics: CESP:F1D11.7

A; Gene: CESP:F1D11.7

A; Map position: 5

A; Introns: 90/3; 185/1; 212/3

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

On protein - protein search, using sw model
Run on: September 20, 2002, 10:27:17 ; Search time 105.99 Seconds
(without alignments) 59.776 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96

Sequence: 1 DSEEDEBHTILTDTELP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTRUS_COMBO.pep:*

2: /cgn2_6/ptodata/2/paa/US06_COMBO.pep:*

3: /cgn2_6/ptodata/2/paa/US07_COMBO.pep:*

4: /cgn2_6/ptodata/2/paa/US08_COMBO.pep:*

5: /cgn2_6/ptodata/2/paa/US081_COMBO.pep:*

6: /cgn2_6/ptodata/2/paa/US082_COMBO.pep:*

7: /cgn2_6/ptodata/2/paa/US084_COMBO.pep:*

8: /cgn2_6/ptodata/2/paa/US085_COMBO.pep:*

9: /cgn2_6/ptodata/2/paa/US086_COMBO.pep:*

10: /cgn2_6/ptodata/2/paa/US087_COMBO.pep:*

11: /cgn2_6/ptodata/2/paa/US088_COMBO.pep:*

12: /cgn2_6/ptodata/2/paa/US089_COMBO.pep:*

13: /cgn2_6/ptodata/2/paa/US090_COMBO.pep:*

14: /cgn2_6/ptodata/2/paa/US091_COMBO.pep:*

15: /cgn2_6/ptodata/2/paa/US092_COMBO.pep:*

16: /cgn2_6/ptodata/2/paa/US093_COMBO.pep:*

17: /cgn2_6/ptodata/2/paa/US094_COMBO.pep:*

18: /cgn2_6/ptodata/2/paa/US095_COMBO.pep:*

19: /cgn2_6/ptodata/2/paa/US096_COMBO.pep:*

20: /cgn2_6/ptodata/2/paa/US097_COMBO.pep:*

21: /cgn2_6/ptodata/2/paa/US098_COMBO.pep:*

22: /cgn2_6/ptodata/2/paa/US099_COMBO.pep:*

23: /cgn2_6/ptodata/2/paa/US100_COMBO.pep:*

24: /cgn2_6/ptodata/2/paa/US101_COMBO.pep:*

25: /cgn2_6/ptodata/2/paa/US60_COMBO.pep:*

26: /cgn2_6/ptodata/2/paa/US60_COMBO.pep:*

RESULT 1
US-08-854-764-7
Sequence 7, Application US/08286530
; GENERAL INFORMATION:
; APPLICANT: Innes, Michael
; APPLICANT: Creasey, Abigail
; TITLE OF INVENTION: Production of Tissue Factor Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/286,530
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saverlaide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0991.001
; TELECOMMUNICATION INFORMATION:

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	96	100.0	18	US-08-286-530-7
2	96	100.0	66	Sequence 7, Appl1
3	96	100.0	66	Sequence 13745, A
4	96	100.0	66	Sequence 18388, A
5	96	100.0	26	Sequence 13745, A
6	96	100.0	66	Sequence 18388, A
7	96	100.0	79	Sequence 13745, A
8	96	100.0	22	Sequence 18388, A
9	96	100.0	66	Sequence 13745, A
10	96	100.0	66	Sequence 18388, A
11	96	100.0	23	Sequence 13745, A
12	96	100.0	152	Sequence 13745, A
13	96	100.0	152	Sequence 13745, A
14	96	100.0	152	Sequence 13745, A
15	96	100.0	161	Sequence 13745, A
16	96	100.0	164	Sequence 13745, A
17	96	100.0	164	Sequence 13745, A
18	96	100.0	164	Sequence 13745, A
19	96	100.0	164	Sequence 13745, A
20	96	100.0	164	Sequence 13745, A
21	96	100.0	210	Sequence 13745, A
22	96	100.0	210	Sequence 13745, A
23	96	100.0	276	Sequence 13745, A
24	96	100.0	276	Sequence 13745, A
25	96	100.0	276	Sequence 13745, A
26	96	100.0	276	Sequence 13745, A
27	96	100.0	276	Sequence 13745, A
28	96	100.0	276	Sequence 13745, A
29	96	100.0	276	Sequence 13745, A
30	96	100.0	291	Sequence 13745, A
31	96	100.0	291	Sequence 13745, A
32	96	100.0	291	Sequence 13745, A
33	96	100.0	291	Sequence 13745, A
34	96	100.0	291	Sequence 13745, A
35	96	100.0	291	Sequence 13745, A
36	96	100.0	291	Sequence 13745, A
37	96	100.0	291	Sequence 13745, A
38	96	100.0	291	Sequence 13745, A
39	96	100.0	291	Sequence 13745, A
40	96	100.0	304	Sequence 13745, A
41	96	100.0	304	Sequence 13745, A
42	96	100.0	304	Sequence 13745, A
43	96	100.0	304	Sequence 13745, A
44	96	100.0	304	Sequence 13745, A
45	96	100.0	304	Sequence 13745, A
46	96	100.0	304	Sequence 13745, A
47	96	100.0	304	Sequence 13745, A
48	96	100.0	304	Sequence 13745, A
49	96	100.0	304	Sequence 13745, A
50	96	100.0	304	Sequence 13745, A
51	96	100.0	304	Sequence 13745, A
52	96	100.0	304	Sequence 13745, A
53	96	100.0	304	Sequence 13745, A
54	96	100.0	304	Sequence 13745, A
55	96	100.0	304	Sequence 13745, A
56	96	100.0	304	Sequence 13745, A
57	96	100.0	304	Sequence 13745, A
58	96	100.0	304	Sequence 13745, A
59	96	100.0	304	Sequence 13745, A
60	96	100.0	304	Sequence 13745, A
61	96	100.0	304	Sequence 13745, A
62	96	100.0	304	Sequence 13745, A
63	96	100.0	304	Sequence 13745, A
64	96	100.0	304	Sequence 13745, A
65	96	100.0	304	Sequence 13745, A
66	96	100.0	304	Sequence 13745, A
67	96	100.0	304	Sequence 13745, A
68	96	100.0	304	Sequence 13745, A
69	96	100.0	304	Sequence 13745, A
70	96	100.0	304	Sequence 13745, A
71	96	100.0	304	Sequence 13745, A
72	96	100.0	304	Sequence 13745, A
73	96	100.0	304	Sequence 13745, A
74	96	100.0	304	Sequence 13745, A
75	96	100.0	304	Sequence 13745, A
76	96	100.0	304	Sequence 13745, A
77	96	100.0	304	Sequence 13745, A
78	96	100.0	304	Sequence 13745, A
79	96	100.0	304	Sequence 13745, A
80	96	100.0	304	Sequence 13745, A
81	96	100.0	304	Sequence 13745, A
82	96	100.0	304	Sequence 13745, A
83	96	100.0	304	Sequence 13745, A
84	96	100.0	304	Sequence 13745, A
85	96	100.0	304	Sequence 13745, A
86	96	100.0	304	Sequence 13745, A
87	96	100.0	304	Sequence 13745, A
88	96	100.0	304	Sequence 13745, A
89	96	100.0	304	Sequence 13745, A
90	96	100.0	304	Sequence 13745, A
91	96	100.0	304	Sequence 13745, A
92	96	100.0	304	Sequence 13745, A
93	96	100.0	304	Sequence 13745, A
94	96	100.0	304	Sequence 13745, A
95	96	100.0	304	Sequence 13745, A
96	96	100.0	304	Sequence 13745, A
97	96	100.0	304	Sequence 13745, A
98	96	100.0	304	Sequence 13745, A
99	96	100.0	304	Sequence 13745, A
100	96	100.0	304	Sequence 13745, A
101	96	100.0	304	Sequence 13745, A
102	96	100.0	304	Sequence 13745, A
103	96	100.0	304	Sequence 13745, A
104	96	100.0	304	Sequence 13745, A
105	96	100.0	304	Sequence 13745, A
106	96	100.0	304	Sequence 13745, A
107	96	100.0	304	Sequence 13745, A
108	96	100.0	304	Sequence 13745, A
109	96	100.0	304	Sequence 13745, A
110	96	100.0	304	Sequence 13745, A
111	96	100.0	304	Sequence 13745, A
112	96	100.0	304	Sequence 13745, A
113	96	100.0	304	Sequence 13745, A
114	96	100.0	304	Sequence 13745, A
115	96	100.0	304	Sequence 13745, A
116	96	100.0	304	Sequence 13745, A
117	96	100.0	304	Sequence 13745, A
118	96	100.0	304	Sequence 13745, A
119	96	100.0	304	Sequence 13745, A
120	96	100.0	304	Sequence 13745, A
121	96	100.0	304	Sequence 13745, A
122	96	100.0	304	Sequence 13745, A
123	96	100.0	304	Sequence 13745, A
124	96	100.0	304	Sequence 13745, A
125	96	100.0	304	Sequence 13745, A
126	96	100.0	304	Sequence 13745, A
127	96	100.0	304	Sequence 13745, A
128	96	100.0	304	Sequence 13745, A
129	96	100.0	304	Sequence 13745, A
130	96	100.0	304	Sequence 13745, A
131	96	100.0	304	Sequence 13745, A
132	96	100.0	304	Sequence 13745, A
133	96	100.0	304	Sequence 13745, A
134	96	100.0	304	Sequence 13745, A
135	96	100.0	304	Sequence 13745, A
136	96	100.0	304	Sequence 13745, A
137	96	100.0	304	Sequence 13745, A
138	96	100.0	304	Sequence 13745, A
139	96	100.0	304	Sequence 13745, A
140	96	100.0	304	Sequence 13745, A
141	96	100.0	304	Sequence 13745, A
142	96	100.0	304	Sequence 13745, A
143	96	100.0	304	Sequence 13745, A
144	96	100.0	304	Sequence 13745, A
145	96	100.0	304	Sequence 13745, A
146	96	100.0	304	Sequence 13745, A
147	96	100.0	304	Sequence 13745, A
148	96	100.0	304	Sequence 13745, A
149	96	100.0	304	Sequence 13745, A
150	96	100.0	304	Sequence 13745, A
151	96	100.0	304	Sequence 13745, A
152	96	100.0	304	Sequence 13745, A
153	96	100.0	304	Sequence 13745, A
154	96	100.0	304	Sequence 13745, A
155	96	100.0	304	Sequence 13745, A
156	96	100.0	304	Sequence 13745, A
157	96	100.0	304	Sequence 13745, A
158	96	100.0	304	Sequence 13745, A
159	96	100.0	304	Sequence 13745, A
160	96	100.0	304	Sequence 13745, A
161	96	100.0	304	Sequence 13745, A
162	96	100.0	304	Sequence 13745, A
163	96	100.0	304	Sequence 13745, A
164	96	100.0	304	Sequence 13745, A
165	96	100.0	304	Sequence 13745, A
166	96	100.0	304	Sequence 13745, A

TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-286-530-7

Query Match 100.0%; Score 96; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DSEEDDEHTTITDTLPP 18
 Db 1 DSEEDDEHTTITDTLPP 18

RESULT 2

US-09-834-366-13745
 Sequence 13745, Application US/09834366
 GENERAL INFORMATION:
 APPLICANT: Bejanin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81.US2.REG
 CURRENT APPLICATION NUMBER: US/09/834,366
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/197,873
 PRIOR FILING DATE: 2000-04-18
 NUMBER OF SEQ ID NOS: 52153
 SOFTWARE: Patent. pm
 SEQ ID NO 13745
 LENGTH: 66
 TYPE: PRT
 ORGANISM: HOMO sapiens
 FEATURE: SIGNAL

NAME/KEY: UNSURE
 LOCATION: 30
 OTHER INFORMATION: Xaa = Ala,Gly
 US-09-834-366-13745

Query Match 100.0%; Score 96; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEEDDEHTTITDTLPP 18
 Db 1 DSEEDDEHTTITDTLPP 18
 29 DSEEDDEHTTITDTLPP 46

RESULT 3
 US-09-834-366-18388
 Sequence 18388, Application US/09834366
 GENERAL INFORMATION:
 APPLICANT: Bejanin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81.US2.REG
 CURRENT APPLICATION NUMBER: US/09/834,366
 CURRENT FILING DATE: 2001-04-13

25

RESULT 4
 US-09-834-366-18388
 Sequence 18388, Application US/09834366
 GENERAL INFORMATION:
 APPLICANT: Bejanin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81.US1.PRO
 CURRENT APPLICATION NUMBER: US/60/197,873
 CURRENT FILING DATE: 2000-04-18
 NUMBER OF SEQ ID NOS: 52153
 SOFTWARE: Patent. pm
 SEQ ID NO 13745
 LENGTH: 66
 TYPE: PRT
 ORGANISM: HOMO sapiens
 FEATURE: SIGNAL
 NAME/KEY: UNSURE
 LOCATION: -28..-1
 NAME/KEY: UNSURE
 LOCATION: 30
 OTHER INFORMATION: Xaa = Ala,Gly
 US-09-834-366-13745

Query Match 100.0%; Score 96; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEEDDEHTTITDTLPP 18
 Db 29 DSEEDDEHTTITDTLPP 46

RESULT 5
 US-09-834-366-18388
 Sequence 18388, Application US/09834366
 GENERAL INFORMATION:
 APPLICANT: Bejanin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81.US1.PRO
 CURRENT APPLICATION NUMBER: US/60/197,873
 CURRENT FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 18386
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 28..71
; US-60-197-873-18388

Query Match 100.0%; Score 96; DB 26; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DSDEDEEHTITDTELP 18
Db 29 DSDEDEEHTITDTELP 46

RESULT 6
US-09-834-366-13738
; Sequence 10, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Mine Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13738
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28..-1
; US-09-834-366-13738

Query Match 100.0%; Score 96; DB 22; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DSDEDEEHTITDTELP 18
Db 29 DSDEDEEHTITDTELP 46

RESULT 7
US-60-197-873-13738
; Sequence 13738, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Mine Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13738

RESULT 8
US-08-276-224-10
; Sequence 10, Application US/08276224
; GENERAL INFORMATION:
; APPLICANT: Norris, Fanny
; APPLICANT: Norris, Kjeld
; APPLICANT: Bjorn, Soren Erik
; APPLICANT: Petersen, Lars Christian
; APPLICANT: Olsen, Ole Hilsted
; TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-56401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOSS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,224
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00002
; FILING DATE: 07-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00340
; FILING DATE: 16-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK93/00005
; FILING DATE: 07-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,605
; FILING DATE: 22-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowmyer, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 3692.210-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-224-10

RESULT 9

us-08-279-753-10 Sequence 10, Application US/08279753

GENERAL INFORMATION:

APPLICANT: 1 DSEDEDEHTTITDTELP 18
1111111111111111
54 DSEDEDEHTTITDTELP 71

TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Novo Nordisk of North America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/279,753A

FILING DATE: 21-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK92/00002

FILING DATE: 07-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK92/00340

FILING DATE: 16-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK93/00005

FILING DATE: 07-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,605

FILING DATE: 22-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gregg, Valeta A.

REGISTRATION NUMBER: 35,127

REFERENCE/DOCKET NUMBER: 3692.220-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-279-753A-10

Query Match 100.0%; Score 96; DB 6; Length 132;

Best Local Similarity 100.0%; Pred. No. 6e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

us-09-924-340-94 Sequence 94, Application US/09924340

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

TITLE OF INVENTION: HUMAN CINAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91 US2 REG

CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT FILING DATE: 2001-08-06

RESULT 10

us-08-279-753A-10

PRIOR APPLICATION NUMBER: US 60/305,456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302,277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298,698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293,574
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: JPatent
 SEQ ID NO: 94
 LENGTH: 152
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: 1..19
 US-09-924-340-94

Query Match 100.0%; Score 96; DB 23; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEBEHTITDTELP 18
 |||||||1111111111111111
 Db 20 DSEDEBEHTITDTELP 37

RESULT 12
 US-09-994-590-94
 Sequence 94, Application US/09994590
 GENERAL INFORMATION:
 APPLICANT: Benjamin, Stephane
 APPLICANT: Tanaka, Hiroaki
 TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 FILE REFERENCE: 91.US3.DIV
 CURRENT APPLICATION NUMBER: US/09/994, 590
 CURRENT FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 09/924, 340
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: PCT/IB01/01715
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/305, 456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302, 277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298, 698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293, 574
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: JPatent
 SEQ ID NO: 94
 LENGTH: 152
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: 1..19
 US-09-994-590-94

RESULT 14
 US-10-000-489-94
 Sequence 94, Application US/10000489
 GENERAL INFORMATION:
 APPLICANT: Benjamin, Stephane
 APPLICANT: Tanaka, Hiroaki
 TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 FILE REFERENCE: 91.US6.DIV
 CURRENT APPLICATION NUMBER: US/10/000,986
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: US 09/924, 340
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: PCT/IB01/01715
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/305, 456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302, 277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298, 698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293, 574
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: JPatent
 SEQ ID NO: 94
 LENGTH: 152
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: 1..19
 US-10-000-489-94

Query Match 100.0%; Score 96; DB 23; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEBEHTITDTELP 18
 |||||||1111111111111111
 Db 20 DSEDEBEHTITDTELP 37

RESULT 13

US-10-000-986-94

Query Match 100.0%; Score 96; DB 24; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DSEDEEHTTITDTELPP 18
 Db 20 DSEDEEHTTITDTELPP 37

RESULT 15

US-09-741-106-19
 Sequence 19, Application US/09741106
 ; GENERAL INFORMATION:
 ; APPLICANT: Innis, Michael
 ; ; Createy, Abia
 ; TITLE OF INVENTION: Chimeric Proteins
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton St.
 ; CITY: Emeryville
 ; STATE: CA USA
 ; COUNTRY: USA
 ; ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/741,106
 FILING DATE: 12-Dec-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/286,521
 FILING DATE: 1994-08-05
 ATTORNEY/AGENT INFORMATION:
 NAME: Savereide, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-741-106-19

Query Match 100.0%; Score 96; DB 21; Length 161;
 Best Local Similarity 100.0%; Pred. No. 7.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DSEDEEHTTITDTELPP 18
 Db 1 DSEDEEHTTITDTELPP 18

Search completed: September 20, 2002, 10:30:30
 Job time: 193 sec

Copyright (c) 1993 - 2000 Compugen Ltd.

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:42 ; Search time 35.94 Seconds
(without alignments)
133.977 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96

Sequence: 1 DSEDEEHHTIDTELLPP 18

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 947138 seqs, 267508082 residues

total number of hits satisfying chosen parameters: 947138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending Patents AA New:*

1: /cgn_2_6/ptodata/2/paa/PCT_NEW_COMBO.pep:*

2: /cgn_2_6/ptodata/2/paa/US06_NEW_COMBO.pep:*

3: /cgn_2_6/ptodata/2/paa/US07_NEW_COMBO.pep:*

4: /cgn_2_6/ptodata/2/paa/US08_NEW_COMBO.pep:*

5: /cgn_2_6/ptodata/2/paa/US09_NEW_COMBO.pep:*

6: /cgn_2_6/ptodata/2/paa/US10_NEW_COMBO.pep:*

7: /cgn_2_6/ptodata/2/paa/US60_NEW_COMBO.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	152	5	US-09-992-600A-94
2	96	100.0	164	5	US-09-992-600A-96
3	96	100.0	231	5	US-09-791-537-120691
4	96	100.0	276	6	US-10-086-176-5
5	96	100.0	276	6	US-10-086-176A-5
6	96	100.0	291	5	US-09-992-600A-48
7	96	100.0	291	5	US-09-992-600A-52
8	96	100.0	304	5	US-09-791-537-101054
9	90	93.8	304	6	US-10-167-351-1
10	90	81.2	91	6	US-10-206-272-546
11	90	81.2	103	6	US-10-206-272-547
12	63	65.6	103	6	US-10-206-272-547
13	57.3	434	6	US-10-179-131-7632	
14	51	53.1	100	6	US-10-211-346-468
15	51	53.1	873	5	US-09-791-537-39142
16	51	53.1	873	5	US-09-791-537-126426
17	50.5	52.6	224	6	US-10-185-050-50
18	50.5	52.6	677	5	US-09-791-537-142737
19	50.5	52.6	1256	5	US-09-791-537-176349
20	50.5	52.6	1256	5	US-09-791-537-107368
21	49.5	51.6	526	6	US-10-104-047-3582
22	49.5	51.6	732	6	US-10-104-047-3582
23	49	51.0	1036	5	US-09-914-64-205
24	47	49.0	300	5	US-09-791-537-1623
25	47	49.0	300	5	US-09-791-537-1623
26	47	49.0	1179	5	US-09-791-537-72053

ALIGNMENTS

RESULT 1

US-09-992-600A-94

Sequence 94, Application US/09992600A

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US4.DIV

CURRENT APPLICATION NUMBER: US/09/992,600A

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 09/924, 340

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/IB01/01715

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305, 456

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/302, 277

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: US 60/298, 698

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 60/293, 574

NUMBER OF SEQ ID NOS: 114

SOFTWARE: JPatent

SEQ ID NO: 94

LENGTH: 152

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SIGNAL

LOCATION: 1..19

US-09-992-600A-94

Query Match Best Local Similarity 100.0%; Score 96; DB 5; Length 152; Matches 18; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHHTIDTELLPP 18

Db 20 DSEDEEHHTIDTELLPP 37

RESULT 2

US-09-992-600A-96

Sequence 95, Application US/09992600A

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNA'S AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91-US4.DLV

CURRENT APPLICATION NUMBER: US/09/992,660A

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US/09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/IB01/01715

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US/60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US/60/302,277

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US/60/298,698

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US/60/293,574

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 114

SOFTWARE: JPatent

SEQ ID NO 96

LENGTH: 164

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: SIGNAL

LOCATION: 1..28

US-09-992-600A-96

Query Match 100.0%; Score 96; DB 5; Length 164;

Best Local Similarity 100.0%; Pred. No. 1.8e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTTIDTELP 18

Db 29 DSEDEDEHTTIDTELP 46

RESULT 3 US-09-791-537-120691

; Sequence 120691, Application US/09/791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; ATTORNEY: Debe, Derek

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

; TITLE OF INVENTION: METHODS OF USE THEREOF

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 120691

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-791-537-120691

Query Match 100.0%; Score 96; DB 5; Length 251;

Best Local Similarity 100.0%; Pred. No. 3e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTTIDTELP 18

Db 29 DSEDEDEHTTIDTELP 46

RESULT 4 US-10-086-176-5

; Sequence 5, Application US/10086176

; GENERAL INFORMATION:

; APPLICANT: Hembrough, Todd

; ATTORNEY: Papathanasiu, Adonia E.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation

; FILE REFERENCE: 05213-026 43170-266780

; CURRENT APPLICATION NUMBER: US/10/086,176

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US/09/766,778

; PRIOR FILING DATE: 2001-01-22

; PRIOR APPLICATION NUMBER: US/09/227,955

; PRIOR FILING DATE: 1999-01-11

; PRIOR APPLICATION NUMBER: US/08/795,850

; PRIOR FILING DATE: 1997-02-06

; PRIOR APPLICATION NUMBER: US/09/130,273

; PRIOR FILING DATE: 1998-08-06

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 276

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; US-10-086-176-5

Query Match 100.0%; Score 96; DB 6; Length 276;

Best Local Similarity 100.0%; Pred. No. 3.3e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEDEHTTIDTELP 18

Db 1 DSEDEDEHTTIDTELP 18

RESULT 6 ;
 US-09-992-600A-52 ;
 Sequence 48, Application US/09992600A ;
 GENERAL INFORMATION:
 APPLICANT: Tanaka, Hiroaki
 TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 FILE REFERENCE: 91.USA.DIV
 CURRENT APPLICATION NUMBER: US/09/992,600A
 CURRENT FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 09/924,340
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: PCT/IB01/01715.
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/305,456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302,277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298,698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293,574
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: JPatent
 SEQ ID NO: 48
 LENGTH: 291
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: 1..28
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: JPatent
 SEQ ID NO: 291
 LENGTH: 291
 TYPE: PRT
 ORGANISM: Homo sapiens
 LOCATION: 1..28
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: JPatent
 SEQ ID NO: 48
 LENGTH: 291
 TYPE: PRT
 ORGANISM: Homo sapiens
 LOCATION: 1..28
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: JPatent

RESULT 7 ;
 US-09-992-600A-52 ;
 Sequence 52, Application US/09992600A ;
 GENERAL INFORMATION:
 APPLICANT: Benjani, Stephane
 APPLICANT: Tanaka, Hiroaki
 TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 FILE REFERENCE: 91.USA.DIV
 CURRENT APPLICATION NUMBER: US/09/992,600A
 CURRENT FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 09/924,340
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: PCT/IB01/01715
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/305,456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302,277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298,698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293,574
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: JPatent
 SEQ ID NO: 52
 LENGTH: 291
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

RESULT 8 ;
 US-09-791-537-101054 ;
 Sequence 101054, Application US/09791537 ;
 GENERAL INFORMATION:
 APPLICANT: Blonomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Danzer, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY METHODS OF USE THEREOF
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 101054
 LENGTH: 304
 TYPE: PRT
 ORGANISM: Homo sapiens
 LOCATION: 1..304
 NUMBER OF SEQ ID NOS: 101054
 SOFTWARE: PatentIn version 3.0

RESULT 9 ;
 US-10-167-351-1 ;
 Sequence 1, Application US/10167351 ;
 GENERAL INFORMATION:
 APPLICANT: DIAK CORP.
 APPLICANT: Markland, William
 APPLICANT: Ladner, Robert C.
 TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
 FILE REFERENCE: DIAK-007.2P US-4
 CURRENT APPLICATION NUMBER: US/10/167,351
 CURRENT FILING DATE: 2002-06-11
 PRIOR APPLICATION NUMBER: 09/638,770
 PRIOR FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: 09/414,878
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: 09/240,136
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: 08/676,124
 PRIOR FILING DATE: 1997-01-07
 PRIOR APPLICATION NUMBER: PCT/US95/00298
 PRIOR FILING DATE: 1995-01-11
 PRIOR APPLICATION NUMBER: 08/208,265
 PRIOR FILING DATE: 1994-03-10
 PRIOR APPLICATION NUMBER: 08/179,658
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 304

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-167-351-1

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 100.0%; Score 96; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Qy 1 DSEDEBEHTITDTEPP 18
Db 29 DSEDEBEHTITDTEPP 46

RESULT 10
; Sequence 15150, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15150
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-791-537-15150

Query Match 93.8%; Score 90; DB 5; Length 304;
Best Local Similarity 94.4%; Pred. No. 2.9e-05;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Qy 1 DSEDEBEHTITDTEPP 18
Db 29 DSEDEBEHTITDTEPP 46

RESULT 11
US-10-206-272-546
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM027C1N
; CURRENT APPLICATION NUMBER: US/10/206,272
; CURRENT FILING DATE: 2002-07-29
; PRIORITY NUMBER: 09/758,445
; PRIORITY NUMBER: 2001-01-11
; PRIORITY NUMBER: 60/179,065
; PRIORITY NUMBER: 2000-01-31
; PRIORITY NUMBER: 60/180,628
; PRIORITY NUMBER: 2000-02-04
; NUMBER OF SEQ ID NOS: 816
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 547
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 93.8%; Score 90; DB 5; Length 304;
Best Local Similarity 94.4%; Pred. No. 2.9e-05;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Qy 1 DSEDEBEHTITDTEPP 18
Db 29 DSEDEBEHTITDTEPP 46

RESULT 11
US-10-206-272-546
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM027C1N
; CURRENT APPLICATION NUMBER: US/10/206,272
; CURRENT FILING DATE: 2002-07-29
; PRIORITY NUMBER: 09/758,445
; PRIORITY NUMBER: 2001-01-11
; PRIORITY NUMBER: 60/179,065
; PRIORITY NUMBER: 2000-01-31
; PRIORITY NUMBER: 60/180,628
; PRIORITY NUMBER: 2000-02-04
; NUMBER OF SEQ ID NOS: 816
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 546
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:28:07 ; Search time 10.34 Seconds
(without alignments)

67.403 Million cell updates/sec

Title: US-08-854-764-7
Perfect score: 96

Sequence: 1 DSEBEDDEHTITTDTELEPP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	304	1	TFPI_HUMAN
2	90	93.8	304	1	TFPI_MACMUI
3	56	58.3	1770	1	TF15_YEAST
4	50	51.0	1394	1	CNGA_BOVIN
5	48	50.0	1085	1	IRPL_YEAST
6	47.5	49.5	1221	1	FBL2_MOUSE
7	47	49.0	300	1	TFPI1_RABBIT
8	46	47.9	2670	1	IP37_RAT
9	44	45.8	504	1	CP31_RAT
10	44	45.8	706	1	TRAIL_MOUSE
11	44	45.8	1	M3KC_RAT	
12	44	45.8	888	1	HMCL_DRONE
13	44	45.8	2175	1	TFPI1_RAT
14	43	44.8	449	1	GATB_MEETH
15	43	44.8	489	1	INGR_HUMAN
16	43	44.8	699	1	HS82_ORYZA
17	43	44.8	1038	1	DPOD_CANAL
18	43	44.8	1103	1	DPOD_MESAU
19	43	44.8	1103	1	DPOD_RAT
20	43	44.8	1105	1	DPOD_MOUSE
21	43	44.8	1106	1	DPOD_BOVIN
22	43	44.8	1107	1	DPOD_HUMAN
23	43	44.8	1234	1	PTP3_MOUSE
24	43	44.8	2016	1	CIN5_HUMAN
25	43	44.8	2019	1	CIMS_RAT
26	43	44.8	2452	1	RPBL_PLATE
27	43	44.8	2863	1	LRBR_HUMAN
28	42.5	44.3	1589	1	DC13_DROME
29	42	44.3	120	1	R31_PICMA
30	42	43.8	302	1	TFPI_RAT
31	42	43.8	396	1	RPA2_HALNI
32	42	43.8	529	1	YABD_SCHPO
33	42	43.8	583	1	PMEU_LYCOP

ALIGNMENTS

RESULT	1
TFPI_HUMAN	
ID	TFPI_HUMAN STANDARD; PRT; 304 AA.
AC	P10646; 095103; 01-JUL-1989 (Rel. 11, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE	(EPI) OR TFPI1 OR LACI.
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_Taxid=9606;
RN	[1]
RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX	MEDLINE=88198127; PubMed=2452157;
RX	RN T.-C. Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.; Raun T., Cloning and characterization of a cDNA coding for the lipoprotein-associated coagulation inhibitor shows that it consists of three tandem Kunitz-type inhibitor domains. J. Biol. Chem. 263:6001-6004(1988).
RX	[2]
RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX	MEDLINE=91129271; PubMed=193173;
RX	RN van der Logt C.P.E., Reitsma P.H., Bartina R.M.; [3]
RX	"Intron-exon organization of the human gene coding for the lipoprotein-associated coagulation inhibitor: the factor Xa dependent inhibitor of the extrinsic pathway of coagulation." R. Biochemistry 30:1571-1577(1991).
RX	RN Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.; Raun T., Cloning and characterization of a cDNA coding for the lipoprotein-associated coagulation inhibitor shows that it consists of three tandem Kunitz-type inhibitor domains. J. Biol. Chem. 263:6001-6004(1988).
RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX	MEDLINE=91161593; PubMed=200245;
RX	RN Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A., Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.; Raun T., Cloning and characterization of a cDNA coding for the lipoprotein-associated coagulation inhibitor shows that it consists of three tandem Kunitz-type inhibitor domains. J. Biol. Chem. 263:6001-6004(1988).
RX	[4]
RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX	MEDLINE=89388722; PubMed=2781520;
RX	RN Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P., Chang J.-Y., Monroe D.M., Roberts H.R.; [5]
RX	"Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein-associated coagulation inhibitor and expression of the encoded protein." Thromb. Res. 55:37-50(1989).
RX	SEQUENCE FROM N.A. (ISOFORM BETA).
RX	RN Chang J.-Y., Monroe D.M., Roberts H.R.; Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RX	[6]
RX	SEQUENCE FROM N.A. (ISOFORM BETA).
RC	TISSUE=Pancreas;

DT 16-OCT-2001 (Rel. 40; last annotation update)
 DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
 DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
 DE (EPI).
 DE (TFPI) OR (TFPI).
 GN
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Macaca.
 OX NEBL_TAXID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=94375417; PubMed=8089087;
 RA Kamei S., Kaneko T., Hamuro T., Fujimoto H., Ishihara M.,
 Yonemura H., Miyamoto S., Funatsu A., Enjoji K., Abumiya T.,
 RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
 factor pathway inhibitor (TFPI); comparison with human TFPI";
 RL J. Biochem. 115:708-714(1994).
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
 A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
 ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
 CC LIPOPROTEINS IN PLASMA.
 CC
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL: S73337; AAB31955.1; -.
 DR RSP: P10646; ITFX.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 3.
 DR PRINTS: PR00759; BASIC_PPAE.
 DR SMART: SM00131; KU; 3.
 DR PROSITE: PS02280; BPTI_KUNITZ_1; 3.
 DR PS50279; BPTI_KUNITZ_2; 3.
 DR SERINE PROTEASE INHIBITOR; GLYCOPROTEIN; REPEAT; BLOOD COAGULATION;
 KW SIGNAL.
 FT SIGNAL 1 28 BY SIMILARITY.
 FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.
 FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1
 FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 12
 FT DOMAIN 217 267 (FACTOR X(A)) BINDING SITE.
 FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 3.
 FT DISULFID 63 87 BY SIMILARITY.
 FT DISULFID 79 100 BY SIMILARITY.
 FT ACT_SITE 64 65 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 125 175 BY SIMILARITY.
 FT DISULFID 134 158 BY SIMILARITY.
 FT DISULFID 150 171 BY SIMILARITY.
 FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 217 267 BY SIMILARITY.
 FT DISULFID 226 250 BY SIMILARITY.
 FT DISULFID 242 263 BY SIMILARITY.
 FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16262B0 CRC64;

Best Local Similarity	Matches	Conservative	Pred.	No. 1.1e-06;	Indels	0;	Gaps	0;
94.4%	17	1	Mismatches	0;	Indels	0;	Gaps	0;
0	1	DSEDEDEHTTIDTEAPP	18	0	0	0	0	0
Db	29	DSEDEDEHTTIDTEAPP	46	0	0	0	0	0
RESULT	3							
RI15_YEAST								
ID	RI15_YEAST							
AC	P43555;							
DT	01-NOV-1995 (Rel. 32, Created)							
DT	01-NOV-1995 (Rel. 32, Last sequence update)							
DT	01-MAR-2002 (Rel. 41, Last annotation update)							
DE	Serine/threonine-protein kinase RIM15 (EC 2.7.1.-).							
GN	RIM15 OR TAK1 OR YFW033C							
OS	Saccharomyces cerevisiae (Baker's yeast).							
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;							
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.							
OX	NEBL_TAXID=4932;							
RN								
RP	SEQUENCE FROM N.A.							
RC	STRAIN=S288C; AB972;							
RX	MEDLINE=95400292; PubMed=670463;							
RA	Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,							
RA	Sasamuna S.-I., Sasamuna M., Tsuchiya Y., Soeda E., Yokoyama K.,							
RA	Yamazaki M., Tashiro H., Eki T.;							
RT	*Analysis of the nucleotide sequence of chromosome VI from							
RT	Saccharomyces cerevisiae*;							
RT	Nat. Genet. 10:261-268(1995).							
RN	[2]							
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.							
RX	MEDLINE=97265402; PubMed=911339;							
RA	Vidan S., Mitchell A.P.;							
RT	*Stimulation of yeast meiotic gene expression by the							
RT	glucose-repressible protein kinase Rim15p*;							
RL	Mol. Cell. Biol. 17:2688-2697(1997).							
RN	[3]							
RP	SEQUENCE FROM N.A.							
RA	Reinders A., Buerckert N., Boller T., Wiemken A., de Virgilio C.,							
RA	Reinigers A., Buerckert N., Boller T., Wiemken A., de Virgilio C.,							
RT	CAMP-dependent protein kinase controls entry							
RT	into stationary phase through the Rim15p protein kinase*;							
RL	Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.							
CC	-1- FUNCTION: INVOLVED IN THE ACTIVATION OF A MEIOTIC GENES ACTIVATION							
CC	-1- PTM: AUTOPHOSPHORYLATED.							
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.							
CC	-1- SIMILARITY: STRONG WITH S. POMBE CEK1.							
CC	-1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.							
CC								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration							
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -							
CC	the European Bioinformatics Institute. There are no restrictions on its							
CC	use by non-profit institutions as long as its content is in no way							
CC	modified and this statement is not removed. Usage by and for commercial							
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
CC								
DR	EMBL: D50617; AAB09206.1; -.							
DR	EMBL: U83459; AAB64088.1; -.							
DR	EMBL: AJ001030; CAA04486.1; -.							
DR	HSSP: 016339; IWFCA.							
DR	SGD: S001861; RIM15.							
DR	InterPro: IPR000961; Euk_Pkinase.							
DR	InterPro: IPR000719; Euk_Pkinase_C.							
DR	InterPro: IPR01789; Response_reg.							
DR	InterPro: IPR002290; Ser_thr_Pkinase.							
DR	Pfam: PF00069; Pkinase; 2.							
DR	Pfam: PF00072; response_reg; 1.							
DR	SMART: SM00448; REC; 1.							
DR	SMART: SM00220; S_TK; 1.							

Query Match

93.8%; Score 90; DB 1; Length 304;

PROSITE: PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50110; RESPONSE_REGULATOR; 1.
 Transferase; Serine/threonine protein kinase; ATP-binding; PROTEIN KINASE.
 PROTEIN KINASE.
 DOMAIN 794 1254 RESPONSE REGULATOR.
 FT DOMAIN 1636 1750 POLY-ASN.
 FT DOMAIN 343 358 POLY-ASN.
 FT DOMAIN 620 624 POLY-SER.
 NP_BIND 800 808 ATP (BY SIMILARITY).
 FT BINDING 823 823 ATP (BY SIMILARITY).
 ACT_SITE 918 918 BY SIMILARITY.
 DOMAIN 975 980 POLY-ASN.
 FT DOMAIN 1213 1218 POLY-GLU.
 FT DOMAIN 1386 1391 POLY-THR.
 SEQUENCE 1770 AA; 196530 MW; DC1064825000FAFF CRC64;

Query Match 58.3%; Score 56; DB 1; Length 1770;
 Best Local Similarity 64.3%; Pred. No. 1.5;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEDDEENHILSDSD 1767
 Db 1754 SEDDEENHILSDSD 1767

RESULT 4
 CNG4_BOVIN STANDARD; PRT: 1394 AA.
 ID CNG4_BOVIN Q28181; Q28082; Q03861;
 AC Q28181; Q28082; Q03861;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 240 kDa protein of rod photoreceptor CNG-channel [Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)].
 GN CNGB1 OR CNGC4.
 OC Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TAXID-9913;
 RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-96090859; PubMed-7516742;
 RA Koerschen H.G., Illing M., Seifert R., Sestl F., Williams A.,
 RA Gotzze C., Colville C., Mueller F., Dose A., Godde M., Molday L.,
 RA Kaupp U.B., Molday R.S.;
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";
 RL Neuron 15: 627-636(1995).
 RN [2] SEQUENCE OF 454-1394 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE-96198098; PubMed-8626431;
 RA Bla M., Zeng X., Ludwig A., Sauter A., Hofmann F.;
 RT Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
 RL J. Biol. Chem. 271:6349-6355(1996).
 RN [3] SEQUENCE OF 1-590 FROM N.A.
 RC TISSUE=Retina;
 RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
 RT Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 CC -1 SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3.
 CC -1 SUBUNIT LOCATION: Integral membrane protein.
 CC -1 ALTERNATIVE PRODUCTS: ISOFORMS; CNG4D (SKOHN HERE), CNG4D AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4D:CNG4E = 20:2:1) IN TESTIS.
 CC -1 TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.

CC -1 SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC PROSITE: PS00100; CNMP_BINDING_1; CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4.
 DR PROSITE: PS00888; CNMP_BINDING_1;
 DR PROSITE: PS00889; CNMP_BINDING_2;
 DR PROSITE: PS50042; CNMP_BINDING_3;
 DR PROSITE: PS50044; CNMP_BINDING_4;
 DR InterPro: IPR00636; CATION_CHAN_NON_LIG.
 DR Ion channel; Ion transport; cAMP-binding; transmembrane; Pfam; PF00227; CNMP_binding_1.
 DR SMART: SM00100; CNMP_1;
 DR SMART: SM00100; CNMP_1;
 DR PROSITE: PS00889; CNMP_BINDING_1;
 DR PROSITE: PS00889; CNMP_BINDING_2;
 DR PROSITE: PS00889; CNMP_BINDING_3;
 DR PROSITE: PS00889; CNMP_BINDING_4;
 DR PROSITE: PS00889; CNMP_BINDING_5;
 DR PROSITE: PS00889; CNMP_BINDING_6;
 DR PROSITE: PS00889; CNMP_BINDING_7;
 DR PROSITE: PS00889; CNMP_BINDING_8;
 DR PROSITE: PS00889; CNMP_BINDING_9;
 DR PROSITE: PS00889; CNMP_BINDING_10;
 DR PROSITE: PS00889; CNMP_BINDING_11;
 DR PROSITE: PS00889; CNMP_BINDING_12;
 DR PROSITE: PS00889; CNMP_BINDING_13;
 DR PROSITE: PS00889; CNMP_BINDING_14;
 DR PROSITE: PS00889; CNMP_BINDING_15;
 DR PROSITE: PS00889; CNMP_BINDING_16;
 DR PROSITE: PS00889; CNMP_BINDING_17;
 DR PROSITE: PS00889; CNMP_BINDING_18;
 DR PROSITE: PS00889; CNMP_BINDING_19;
 DR PROSITE: PS00889; CNMP_BINDING_20;
 DR PROSITE: PS00889; CNMP_BINDING_21;
 DR PROSITE: PS00889; CNMP_BINDING_22;
 DR PROSITE: PS00889; CNMP_BINDING_23;
 DR PROSITE: PS00889; CNMP_BINDING_24;
 DR PROSITE: PS00889; CNMP_BINDING_25;
 DR PROSITE: PS00889; CNMP_BINDING_26;
 DR PROSITE: PS00889; CNMP_BINDING_27;
 DR PROSITE: PS00889; CNMP_BINDING_28;
 DR PROSITE: PS00889; CNMP_BINDING_29;
 DR PROSITE: PS00889; CNMP_BINDING_30;
 DR PROSITE: PS00889; CNMP_BINDING_31;
 DR PROSITE: PS00889; CNMP_BINDING_32;
 DR PROSITE: PS00889; CNMP_BINDING_33;
 DR PROSITE: PS00889; CNMP_BINDING_34;
 DR PROSITE: PS00889; CNMP_BINDING_35;
 DR PROSITE: PS00889; CNMP_BINDING_36;
 DR PROSITE: PS00889; CNMP_BINDING_37;
 DR PROSITE: PS00889; CNMP_BINDING_38;
 DR PROSITE: PS00889; CNMP_BINDING_39;
 DR PROSITE: PS00889; CNMP_BINDING_40;
 DR PROSITE: PS00889; CNMP_BINDING_41;
 DR PROSITE: PS00889; CNMP_BINDING_42;
 DR PROSITE: PS00889; CNMP_BINDING_43;
 DR PROSITE: PS00889; CNMP_BINDING_44;
 DR PROSITE: PS00889; CNMP_BINDING_45;
 DR PROSITE: PS00889; CNMP_BINDING_46;
 DR PROSITE: PS00889; CNMP_BINDING_47;
 DR PROSITE: PS00889; CNMP_BINDING_48;
 DR PROSITE: PS00889; CNMP_BINDING_49;
 DR PROSITE: PS00889; CNMP_BINDING_50;
 DR PROSITE: PS00889; CNMP_BINDING_51;
 DR PROSITE: PS00889; CNMP_BINDING_52;
 DR PROSITE: PS00889; CNMP_BINDING_53;
 DR PROSITE: PS00889; CNMP_BINDING_54;
 DR PROSITE: PS00889; CNMP_BINDING_55;
 DR PROSITE: PS00889; CNMP_BINDING_56;
 DR PROSITE: PS00889; CNMP_BINDING_57;
 DR PROSITE: PS00889; CNMP_BINDING_58;
 DR PROSITE: PS00889; CNMP_BINDING_59;
 DR PROSITE: PS00889; CNMP_BINDING_60;
 DR PROSITE: PS00889; CNMP_BINDING_61;
 DR PROSITE: PS00889; CNMP_BINDING_62;
 DR PROSITE: PS00889; CNMP_BINDING_63;
 DR PROSITE: PS00889; CNMP_BINDING_64;
 DR PROSITE: PS00889; CNMP_BINDING_65;
 DR PROSITE: PS00889; CNMP_BINDING_66;
 DR PROSITE: PS00889; CNMP_BINDING_67;
 DR PROSITE: PS00889; CNMP_BINDING_68;
 DR PROSITE: PS00889; CNMP_BINDING_69;
 DR PROSITE: PS00889; CNMP_BINDING_70;
 DR PROSITE: PS00889; CNMP_BINDING_71;
 DR PROSITE: PS00889; CNMP_BINDING_72;
 DR PROSITE: PS00889; CNMP_BINDING_73;
 DR PROSITE: PS00889; CNMP_BINDING_74;
 DR PROSITE: PS00889; CNMP_BINDING_75;
 DR PROSITE: PS00889; CNMP_BINDING_76;
 DR PROSITE: PS00889; CNMP_BINDING_77;
 DR PROSITE: PS00889; CNMP_BINDING_78;
 DR PROSITE: PS00889; CNMP_BINDING_79;
 DR PROSITE: PS00889; CNMP_BINDING_80;
 DR PROSITE: PS00889; CNMP_BINDING_81;
 DR PROSITE: PS00889; CNMP_BINDING_82;
 DR PROSITE: PS00889; CNMP_BINDING_83;
 DR PROSITE: PS00889; CNMP_BINDING_84;
 DR PROSITE: PS00889; CNMP_BINDING_85;
 DR PROSITE: PS00889; CNMP_BINDING_86;
 DR PROSITE: PS00889; CNMP_BINDING_87;
 DR PROSITE: PS00889; CNMP_BINDING_88;
 DR PROSITE: PS00889; CNMP_BINDING_89;
 DR PROSITE: PS00889; CNMP_BINDING_90;
 DR PROSITE: PS00889; CNMP_BINDING_91;
 DR PROSITE: PS00889; CNMP_BINDING_92;
 DR PROSITE: PS00889; CNMP_BINDING_93;
 DR PROSITE: PS00889; CNMP_BINDING_94;
 DR PROSITE: PS00889; CNMP_BINDING_95;
 DR PROSITE: PS00889; CNMP_BINDING_96;
 DR PROSITE: PS00889; CNMP_BINDING_97;
 DR PROSITE: PS00889; CNMP_BINDING_98;
 DR PROSITE: PS00889; CNMP_BINDING_99;
 DR PROSITE: PS00889; CNMP_BINDING_100;
 DR PROSITE: PS00889; CNMP_BINDING_101;
 DR PROSITE: PS00889; CNMP_BINDING_102;
 DR PROSITE: PS00889; CNMP_BINDING_103;
 DR PROSITE: PS00889; CNMP_BINDING_104;
 DR PROSITE: PS00889; CNMP_BINDING_105;
 DR PROSITE: PS00889; CNMP_BINDING_106;
 DR PROSITE: PS00889; CNMP_BINDING_107;
 DR PROSITE: PS00889; CNMP_BINDING_108;
 DR PROSITE: PS00889; CNMP_BINDING_109;
 DR PROSITE: PS00889; CNMP_BINDING_110;
 DR PROSITE: PS00889; CNMP_BINDING_111;
 DR PROSITE: PS00889; CNMP_BINDING_112;
 DR PROSITE: PS00889; CNMP_BINDING_113;
 DR PROSITE: PS00889; CNMP_BINDING_114;
 DR PROSITE: PS00889; CNMP_BINDING_115;
 DR PROSITE: PS00889; CNMP_BINDING_116;
 DR PROSITE: PS00889; CNMP_BINDING_117;
 DR PROSITE: PS00889; CNMP_BINDING_118;
 DR PROSITE: PS00889; CNMP_BINDING_119;
 DR PROSITE: PS00889; CNMP_BINDING_120;
 DR PROSITE: PS00889; CNMP_BINDING_121;
 DR PROSITE: PS00889; CNMP_BINDING_122;
 DR PROSITE: PS00889; CNMP_BINDING_123;
 DR PROSITE: PS00889; CNMP_BINDING_124;
 DR PROSITE: PS00889; CNMP_BINDING_125;
 DR PROSITE: PS00889; CNMP_BINDING_126;
 DR PROSITE: PS00889; CNMP_BINDING_127;
 DR PROSITE: PS00889; CNMP_BINDING_128;
 DR PROSITE: PS00889; CNMP_BINDING_129;
 DR PROSITE: PS00889; CNMP_BINDING_130;
 DR PROSITE: PS00889; CNMP_BINDING_131;
 DR PROSITE: PS00889; CNMP_BINDING_132;
 DR PROSITE: PS00889; CNMP_BINDING_133;
 DR PROSITE: PS00889; CNMP_BINDING_134;
 DR PROSITE: PS00889; CNMP_BINDING_135;
 DR PROSITE: PS00889; CNMP_BINDING_136;
 DR PROSITE: PS00889; CNMP_BINDING_137;
 DR PROSITE: PS00889; CNMP_BINDING_138;
 DR PROSITE: PS00889; CNMP_BINDING_139;
 DR PROSITE: PS00889; CNMP_BINDING_140;
 DR PROSITE: PS00889; CNMP_BINDING_141;
 DR PROSITE: PS00889; CNMP_BINDING_142;
 DR PROSITE: PS00889; CNMP_BINDING_143;
 DR PROSITE: PS00889; CNMP_BINDING_144;
 DR PROSITE: PS00889; CNMP_BINDING_145;
 DR PROSITE: PS00889; CNMP_BINDING_146;
 DR PROSITE: PS00889; CNMP_BINDING_147;
 DR PROSITE: PS00889; CNMP_BINDING_148;
 DR PROSITE: PS00889; CNMP_BINDING_149;
 DR PROSITE: PS00889; CNMP_BINDING_150;
 DR PROSITE: PS00889; CNMP_BINDING_151;
 DR PROSITE: PS00889; CNMP_BINDING_152;
 DR PROSITE: PS00889; CNMP_BINDING_153;
 DR PROSITE: PS00889; CNMP_BINDING_154;
 DR PROSITE: PS00889; CNMP_BINDING_155;
 DR PROSITE: PS00889; CNMP_BINDING_156;
 DR PROSITE: PS00889; CNMP_BINDING_157;
 DR PROSITE: PS00889; CNMP_BINDING_158;
 DR PROSITE: PS00889; CNMP_BINDING_159;
 DR PROSITE: PS00889; CNMP_BINDING_160;
 DR PROSITE: PS00889; CNMP_BINDING_161;
 DR PROSITE: PS00889; CNMP_BINDING_162;
 DR PROSITE: PS00889; CNMP_BINDING_163;
 DR PROSITE: PS00889; CNMP_BINDING_164;
 DR PROSITE: PS00889; CNMP_BINDING_165;
 DR PROSITE: PS00889; CNMP_BINDING_166;
 DR PROSITE: PS00889; CNMP_BINDING_167;
 DR PROSITE: PS00889; CNMP_BINDING_168;
 DR PROSITE: PS00889; CNMP_BINDING_169;
 DR PROSITE: PS00889; CNMP_BINDING_170;
 DR PROSITE: PS00889; CNMP_BINDING_171;
 DR PROSITE: PS00889; CNMP_BINDING_172;
 DR PROSITE: PS00889; CNMP_BINDING_173;
 DR PROSITE: PS00889; CNMP_BINDING_174;
 DR PROSITE: PS00889; CNMP_BINDING_175;
 DR PROSITE: PS00889; CNMP_BINDING_176;
 DR PROSITE: PS00889; CNMP_BINDING_177;
 DR PROSITE: PS00889; CNMP_BINDING_178;
 DR PROSITE: PS00889; CNMP_BINDING_179;
 DR PROSITE: PS00889; CNMP_BINDING_180;
 DR PROSITE: PS00889; CNMP_BINDING_181;
 DR PROSITE: PS00889; CNMP_BINDING_182;
 DR PROSITE: PS00889; CNMP_BINDING_183;
 DR PROSITE: PS00889; CNMP_BINDING_184;
 DR PROSITE: PS00889; CNMP_BINDING_185;
 DR PROSITE: PS00889; CNMP_BINDING_186;
 DR PROSITE: PS00889; CNMP_BINDING_187;
 DR PROSITE: PS00889; CNMP_BINDING_188;
 DR PROSITE: PS00889; CNMP_BINDING_189;
 DR PROSITE: PS00889; CNMP_BINDING_190;
 DR PROSITE: PS00889; CNMP_BINDING_191;
 DR PROSITE: PS00889; CNMP_BINDING_192;
 DR PROSITE: PS00889; CNMP_BINDING_193;
 DR PROSITE: PS00889; CNMP_BINDING_194;
 DR PROSITE: PS00889; CNMP_BINDING_195;
 DR PROSITE: PS00889; CNMP_BINDING_196;
 DR PROSITE: PS00889; CNMP_BINDING_197;
 DR PROSITE: PS00889; CNMP_BINDING_198;
 DR PROSITE: PS00889; CNMP_BINDING_199;
 DR PROSITE: PS00889; CNMP_BINDING_200;
 DR PROSITE: PS00889; CNMP_BINDING_201;
 DR PROSITE: PS00889; CNMP_BINDING_202;
 DR PROSITE: PS00889; CNMP_BINDING_203;
 DR PROSITE: PS00889; CNMP_BINDING_204;
 DR PROSITE: PS00889; CNMP_BINDING_205;
 DR PROSITE: PS00889; CNMP_BINDING_206;
 DR PROSITE: PS00889; CNMP_BINDING_207;
 DR PROSITE: PS00889; CNMP_BINDING_208;
 DR PROSITE: PS00889; CNMP_BINDING_209;
 DR PROSITE: PS00889; CNMP_BINDING_210;
 DR PROSITE: PS00889; CNMP_BINDING_211;
 DR PROSITE: PS00889; CNMP_BINDING_212;
 DR PROSITE: PS00889; CNMP_BINDING_213;
 DR PROSITE: PS00889; CNMP_BINDING_214;
 DR PROSITE: PS00889; CNMP_BINDING_215;
 DR PROSITE: PS00889; CNMP_BINDING_216;
 DR PROSITE: PS00889; CNMP_BINDING_217;
 DR PROSITE: PS00889; CNMP_BINDING_218;
 DR PROSITE: PS00889; CNMP_BINDING_219;
 DR PROSITE: PS00889; CNMP_BINDING_220;
 DR PROSITE: PS00889; CNMP_BINDING_221;
 DR PROSITE: PS00889; CNMP_BINDING_222;
 DR PROSITE: PS00889; CNMP_BINDING_223;
 DR PROSITE: PS00889; CNMP_BINDING_224;
 DR PROSITE: PS00889; CNMP_BINDING_225;
 DR PROSITE: PS00889; CNMP_BINDING_226;
 DR PROSITE: PS00889; CNMP_BINDING_227;
 DR PROSITE: PS00889; CNMP_BINDING_228;
 DR PROSITE: PS00889; CNMP_BINDING_229;
 DR PROSITE: PS00889; CNMP_BINDING_230;
 DR PROSITE: PS00889; CNMP_BINDING_231;
 DR PROSITE: PS00889; CNMP_BINDING_232;
 DR PROSITE: PS00889; CNMP_BINDING_233;
 DR PROSITE: PS00889; CNMP_BINDING_234;
 DR PROSITE: PS00889; CNMP_BINDING_235;
 DR PROSITE: PS00889; CNMP_BINDING_236;
 DR PROSITE: PS00889; CNMP_BINDING_237;
 DR PROSITE: PS00889; CNMP_BINDING_238;
 DR PROSITE: PS00889; CNMP_BINDING_239;
 DR PROSITE: PS00889; CNMP_BINDING_240;
 DR PROSITE: PS00889; CNMP_BINDING_241;
 DR PROSITE: PS00889; CNMP_BINDING_242;
 DR PROSITE: PS00889; CNMP_BINDING_243;
 DR PROSITE: PS00889; CNMP_BINDING_244;
 DR PROSITE: PS00889; CNMP_BINDING_245;
 DR PROSITE: PS00889; CNMP_BINDING_246;
 DR PROSITE: PS00889; CNMP_BINDING_247;
 DR PROSITE: PS00889; CNMP_BINDING_248;
 DR PROSITE: PS00889; CNMP_BINDING_249;
 DR PROSITE: PS00889; CNMP_BINDING_250;
 DR PROSITE: PS00889; CNMP_BINDING_251;
 DR PROSITE: PS00889; CNMP_BINDING_252;
 DR PROSITE: PS00889; CNMP_BINDING_253;
 DR PROSITE: PS00889; CNMP_BINDING_254;
 DR PROSITE: PS00889; CNMP_BINDING_255;
 DR PROSITE: PS00889; CNMP_BINDING_256;
 DR PROSITE: PS00889; CNMP_BINDING_257;
 DR PROSITE: PS00889; CNMP_BINDING_258;
 DR PROSITE: PS00889; CNMP_BINDING_259;
 DR PROSITE: PS00889; CNMP_BINDING_260;
 DR PROSITE: PS00889; CNMP_BINDING_261;
 DR PROSITE: PS00889; CNMP_BINDING_262;
 DR PROSITE: PS00889; CNMP_BINDING_263;
 DR PROSITE: PS00889; CNMP_BINDING_264;
 DR PROSITE: PS00889; CNMP_BINDING_265;
 DR PROSITE: PS00889; CNMP_BINDING_266;
 DR PROSITE: PS00889; CNMP_BINDING_267;
 DR PROSITE: PS00889; CNMP_BINDING_268;
 DR PROSITE: PS00889; CNMP_BINDING_269;
 DR PROSITE: PS00889; CNMP_BINDING_270;
 DR PROSITE: PS00889; CNMP_BINDING_271;
 DR PROSITE: PS00889; CNMP_BINDING_272;
 DR PROSITE: PS00889; CNMP_BINDING_273;
 DR PROSITE: PS00889; CNMP_BINDING_274;
 DR PROSITE: PS00889; CNMP_BINDING_275;
 DR PROSITE: PS00889; CNMP_BINDING_276;
 DR PROSITE: PS00889; CNMP_BINDING_277;
 DR PROSITE: PS00889; CNMP_BINDING_278;
 DR PROSITE: PS00889; CNMP_BINDING_279;
 DR PROSITE: PS00889; CNMP_BINDING_280;
 DR PROSITE: PS00889; CNMP_BINDING_281;
 DR PROSITE: PS00889; CNMP_BINDING_282;
 DR PROSITE: PS00889; CNMP_BINDING_283;
 DR PROSITE: PS00889; CNMP_BINDING_284;
 DR PROSITE: PS00889; CNMP_BINDING_285;
 DR PROSITE: PS00889; CNMP_BINDING_286;
 DR PROSITE: PS00889; CNMP_BINDING_287;
 DR PROSITE: PS00889; CNMP_BINDING_288;
 DR PROSITE: PS00889; CNMP_BINDING_289;
 DR PROSITE: PS00889; CNMP_BINDING_290;
 DR PROSITE: PS00889; CNMP_BINDING_291;
 DR PROSITE: PS00889; CNMP_BINDING_292;
 DR PROSITE: PS00889; CNMP_BINDING_293;
 DR PROSITE: PS00889; CNMP_BINDING_294;
 DR PROSITE: PS00889; CNMP_BINDING_295;
 DR PROSITE: PS00889; CNMP_BINDING_296;
 DR PROSITE: PS00889; CNMP_BINDING_297;
 DR PROSITE: PS00889; CNMP_BINDING_298;
 DR PROSITE: PS00889; CNMP_BINDING_299;
 DR PROSITE: PS00889; CNMP_BINDING_300;
 DR PROSITE: PS00889; CNMP_BINDING_301;
 DR PROSITE: PS00889; CNMP_BINDING_302;
 DR PROSITE: PS00889; CNMP_BINDING_303;
 DR PROSITE: PS00889; CNMP_BINDING_304;
 DR PROSITE: PS00889; CNMP_BINDING_305;
 DR PROSITE: PS00889; CNMP_BINDING_306;
 DR PROSITE: PS00889; CNMP_BINDING_307;
 DR PROSITE: PS00889; CNMP_BINDING_308;
 DR PROSITE: PS00889; CNMP_BINDING_309;
 DR PROSITE: PS00889; CNMP_BINDING_310;
 DR PROSITE: PS00889; CNMP_BINDING_311;
 DR PROSITE: PS00889; CNMP_BINDING_312;
 DR PROSITE: PS00889; CNMP_BINDING_313;
 DR PROSITE: PS00889; CNMP_BINDING_314;
 DR PROSITE: PS00889; CNMP_BINDING_315;
 DR PROSITE: PS00889; CNMP_BINDING_316;
 DR PROSITE: PS00889; CNMP_BINDING_317;
 DR PROSITE: PS00889; CNMP_BINDING_318;
 DR PROSITE: PS00889; CNMP_BINDING_319;
 DR PROSITE: PS00889; CNMP_BINDING_320;
 DR PROSITE: PS00889; CNMP_BINDING_321;
 DR PROSITE: PS00889; CNMP_BINDING_322;
 DR PROSITE: PS00889; CNMP_BINDING_323;
 DR PROSITE: PS00889; CNMP_BINDING_324;
 DR PROSITE: PS00889; CNMP_BINDING_325;
 DR PROSITE: PS00889; CNMP_BINDING_326;
 DR PROSITE: PS00889; CNMP_BINDING_327;
 DR PROSITE: PS00889; CNMP_BINDING_328;
 DR PROSITE: PS00889; CNMP_BINDING_329;
 DR PROSITE: PS00889; CNMP_BINDING_330;
 DR PROSITE: PS00889; CNMP_BINDING_331;
 DR PROSITE: PS00889; CNMP_BINDING_332;
 DR PROSITE: PS00889; CNMP_BINDING_333;
 DR PROSITE: PS00889; CNMP_BINDING_334;
 DR PROSITE: PS00889; CNMP_BINDING_335;
 DR PROSITE: PS00889; CNMP_BINDING_336;
 DR PROSITE: PS00889; CNMP_BINDING_337;
 DR PROSITE: PS00889; CNMP_BINDING_338;
 DR PROSITE: PS00889; CNMP_BINDING_339;
 DR PROSITE: PS00889; CNMP_BINDING_340;
 DR PROSITE: PS00889; CNMP_BINDING_341;
 DR PROSITE: PS00889; CNMP_BINDING_342;
 DR PROSITE: PS00889; CNMP_BINDING_343;
 DR PROSITE: PS00889; CNMP_BINDING_344;
 DR PROSITE: PS00889; CNMP_BINDING_345;
 DR PROSITE: PS00889; CNMP_BINDING_346;
 DR PROSITE: PS00889; CNMP_BINDING_347;
 DR PROSITE: PS00889; CNMP_BINDING_348;
 DR PROSITE: PS00889; CNMP_BINDING_349;
 DR PROSITE: PS00889; CNMP_BINDING_350;
 DR PROSITE: PS00889; CNMP_BINDING_351;
 DR PROSITE: PS00889; CNMP_BINDING_352;
 DR PROSITE: PS00889; CNMP_BINDING_353;
 DR PROSITE: PS00889; CNMP_BINDING_354;
 DR PROSITE: PS00889; CNMP_BINDING_355;
 DR PROSITE: PS00889; CNMP_BINDING_356;
 DR PROSITE: PS00889; CNMP_BINDING_357;
 DR PROSITE: PS00889; CNMP_BINDING_358;
 DR PROSITE: PS00889; CNMP_BINDING_359;
 DR PROSITE: PS00889; CNMP_BINDING_360;
 DR PROSITE: PS00889; CNMP_BINDING_361;
 DR PROSITE: PS00889; CNMP_BINDING_362;
 DR PROSITE: PS00889; CNMP_BINDING_363;
 DR PROSITE: PS00889; CNMP_BINDING_364;
 DR PROSITE: PS00889; CNMP_BINDING_365;
 DR PROSITE: PS00889; CNMP_BINDING_366;
 DR PROSITE: PS00889; CNMP_BINDING_367;
 DR PROSITE: PS00889; CNMP_BINDING_368;
 DR PROSITE: PS00889; CNMP_BINDING_369;
 DR PROSITE: PS00889; CNMP_BINDING_370;
 DR PROSITE: PS00889; CNMP_BINDING_371;
 DR PROSITE: PS00889; CNMP_BINDING_372;
 DR PROSITE: PS00889; CNMP_BINDING_373;
 DR PROSITE: PS00889; CNMP_BINDING_374;
 DR PROSITE: PS00889; CNMP_BINDING_375;
 DR PROSITE: PS00889; CNMP_BINDING_376;
 DR PROSITE: PS00889; CNMP_BINDING_377;
 DR PROSITE: PS00889; CNMP_BINDING_378;
 DR PROSITE: PS00889; CNMP_BINDING_379;
 DR PROSITE: PS00889; CNMP_BINDING_380;
 DR PROSITE: PS00889; CNMP_BINDING_381;
 DR PROSITE: PS00889; CNMP_BINDING_382;
 DR PROSITE: PS00889; CNMP_BINDING_383;
 DR PROSITE: PS00889; CNMP_BINDING_384;
 DR PROSITE: PS00889; CNMP_BINDING_385;
 DR PROSITE: PS00889; CNMP_BINDING_386;
 DR PROSITE: PS00889; CNMP_BINDING_387;
 DR PROSITE: PS00889; CNMP_BINDING_388;
 DR PROSITE: PS00889; CNMP_BINDING_389;
 DR PROSITE: PS00889; CNMP_BINDING_390;
 DR PROSITE: PS00889; CNMP_BINDING_391;
 DR PROSITE: PS00889; CNMP_BINDING_392;
 DR PROSITE: PS00889; CNMP_BINDING_393;
 DR PROSITE: PS00889; CNMP_BINDING_394;
 DR PROSITE: PS00889; CNMP_BINDING_395;
 DR PROSITE: PS00889; CNMP_BINDING_396;
 DR PROSITE: PS00889; CNMP_BINDING_397;
 DR PROSITE: PS00889; CNMP_BINDING_398;
 DR PROSITE: PS00889; CNMP_BINDING_399;
 DR PROSITE: PS00889; CNMP_BINDING_400;
 DR PROSITE: PS00889; CNMP_BINDING_401;
 DR PROSITE: PS00889; CNMP_BINDING_402;
 DR PROSITE: PS00889; CNMP_BINDING_403;
 DR PROSITE: PS00889; CNMP_BINDING_404;
 DR PROSITE: PS00889; CNMP_BINDING_405;
 DR PROSITE: PS00889; CNMP_BINDING_406;
 DR PROSITE: PS00889; CNMP_BINDING_407;
 DR PROSITE: PS00889; CNMP_BINDING_408;
 DR PROSITE: PS00889; CNMP_BINDING_409;
 DR PROSITE: PS00889; CNMP_BINDING_410;
 DR PROSITE: PS00889; CNMP_BINDING_411;
 DR PROSITE: PS00889; CNMP_BINDING_412;
 DR PROSITE: PS00889; CNMP_BINDING_413;
 DR PROSITE: PS00889; CNMP_BINDING_414;
 DR PROSITE: PS00889; CNMP_BINDING_415;
 DR PROSITE: PS00889; CNMP_BINDING_416;
 DR PROSITE: PS00889; CNMP_BINDING_417;
 DR PROSITE: PS00889; CNMP_BINDING_418;
 DR PROSITE: PS00889; CNMP_BINDING_419;
 DR PROSITE: PS00889; CNMP_BINDING_420;
 DR PROSITE: PS00889; CNMP_BINDING_421;
 DR PROSITE: PS00889; CNMP_BINDING_422;
 DR PROSITE: PS00889; CNMP_BINDING_423;
 DR PROSITE: PS00889; CNMP_BINDING_424;
 DR PROSITE: PS00889; CNMP_BINDING_425;
 DR PROSITE: PS00889; CNMP_BINDING_426;
 DR PROSITE: PS00889; CNMP_BINDING_427;
 DR PROSITE: PS00889; CNMP_BINDING_428;
 DR PROSITE: PS00889; CNMP_BINDING_429;
 DR PROSITE: PS00889; CNMP_BINDING_430;
 DR PROSITE: PS00889; CNMP_BINDING_431;
 DR PROSITE: PS00889; CNMP_BINDING_432;
 DR PROSITE: PS00889; CNMP_BINDING_433;
 DR PROSITE: PS00889; CNMP_BINDING_434;
 DR PROSITE: PS00889; CNMP_BINDING_435;

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE IFH1 protein (RRP3 protein).
 DE IFH1 OR RRP3, OR YLR083C OR L8083.9.
 RA MEDLINE-95304839; PubMed-7785326;
 RA MEDLINE-95304839; PubMed-7785326;
 RA "Structure and expression of fibulin-2, a novel extracellular matrix
 protein with multiple EGF-like repeats and consensus motifs for
 protein kinase C and calcium binding."
 RA Cell Biol. 123:1269-1277(1993).
 RL [1] FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN-FL100;
 RX MELDINE-95304839; PubMed-7785326;
 RA Cherel I., Thuriaux P.;
 RT "The IFH1 gene product: interacts with a fork head protein in
 Saccharomyces cerevisiae";
 RL Yeast-1:261-270(1995).
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
 RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
 RA Mardi E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
 RA Riffen L., Riles L., Tach A., Traversakis E., Vignati D.,
 RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 -I- FUNCTION: CONTROLS THE PRE-RNA PROCESSING MACHINERY IN
 CONJUNCTION WITH FHL1. COULD CONVERT FHL1 FROM A REPRESSOR
 TO AN ACTIVATOR.
 -I- SUBCELLULAR LOCATION: NUCLEAR (probable).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL; X75285; CAN53040.1;
 DR EMBL; AF135253; ADD34456.1; JOINED.
 DR EMBL; AF135239; ADD34456.1; JOINED.
 DR EMBL; AF135240; ADD34456.1; JOINED.
 DR EMBL; AF135241; ADD34456.1; JOINED.
 DR EMBL; AF135242; ADD34456.1; JOINED.
 DR EMBL; AF135243; ADD34456.1; JOINED.
 DR EMBL; AF135244; ADD34456.1; JOINED.
 DR EMBL; AF135245; ADD34456.1; JOINED.
 DR EMBL; AF135246; ADD34456.1; JOINED.
 DR EMBL; AF135247; ADD34456.1; JOINED.
 DR EMBL; AF135248; ADD34456.1; JOINED.
 DR EMBL; AF135249; ADD34456.1; JOINED.
 DR EMBL; AF135250; ADD34456.1; JOINED.
 DR EMBL; AF135251; ADD34456.1; JOINED.
 DR EMBL; AF135252; ADD34456.1; JOINED.
 DR PIR; A49457; A49457.
 DR HSSP; P07204; IFGD.
 DR MGI; MGI:95488; Fbn2.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx-hydroxyl.
 DR InterPro; IPR000501; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR Pfam; PF00008; EGF_6.
 DR SMART; SM00104; ANRTO; 3.
 DR SMART; SM00179; EGF_Ca; 9.
 DR SMART; SM00001; EGF_like; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF_Ca; 10.
 DR Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 KW Calcium-binding; Alternative splicing; Repeat.
 FT SIGNAL; 1 26
 FT CHAIN 27 1221 FIBULIN-2.
 FT DOMAIN 27 434 N.
 FT DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).
 RC

FT	DOMAIN	177	434	SUBDOMAIN NB (CYS-FREE).	RESULT 7
FT	DOMAIN	435	477	ANAPHYLATOXIN-LIKE 1.	TPPI_RABBIT STANDARD;
FT	DOMAIN	510	510	ANAPHYLATOXIN-LIKE 2.	ID TPPI_RABBIT STANDARD;
FT	DOMAIN	511	543	ANAPHYLATOXIN-LIKE 3.	ID TPPI_RABBIT STANDARD;
FT	DOMAIN	594	635	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).	AC P19761; Q28828;
FT	DOMAIN	669	708	EGF-LIKE 2.	AC P19761; Q28828;
FT	DOMAIN	709	755	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).	DT 01-AUG-1991 (Rel. 17, Created)
FT	DOMAIN	756	800	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).	DT 01-AUG-1992 (Rel. 23, Last sequence update)
FT	DOMAIN	801	846	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).	DT 16-OCT-2001 (Rel. 40, Last annotation update)
FT	DOMAIN	847	894	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).	DT Tissue factor pathway inhibitor Precursor (TPPI) (Lipoprotein- associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor) (EPI).
FT	DOMAIN	895	937	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).	DE (EPI).
FT	DOMAIN	938	979	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).	DE (EPI).
FT	DOMAIN	980	1018	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).	DE (EPI).
FT	DOMAIN	1019	1061	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).	DE (EPI).
FT	DOMAIN	1062	1106	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).	DE (EPI).
FT	DOMAIN	1111	1221	DOMAIN XII.	DE (EPI).
FT	SITE	421	423	CELL ATTACHMENT SITE (POTENTIAL).	DE (EPI).
FT	DISULFID	435	462	BY SIMILARITY.	DE (EPI).
FT	DISULFID	436	469	BY SIMILARITY.	DE (EPI).
FT	DISULFID	449	470	BY SIMILARITY.	DE (EPI).
FT	DISULFID	479	509	BY SIMILARITY.	DE (EPI).
FT	DISULFID	492	509	BY SIMILARITY.	DE (EPI).
FT	DISULFID	511	535	BY SIMILARITY.	DE (EPI).
FT	DISULFID	512	542	BY SIMILARITY.	DE (EPI).
FT	DISULFID	525	543	BY SIMILARITY.	DE (EPI).
FT	DISULFID	598	610	BY SIMILARITY.	DE (EPI).
FT	DISULFID	606	619	BY SIMILARITY.	DE (EPI).
FT	DISULFID	621	634	BY SIMILARITY.	DE (EPI).
FT	DISULFID	673	683	BY SIMILARITY.	DE (EPI).
FT	DISULFID	679	692	BY SIMILARITY.	DE (EPI).
FT	DISULFID	694	707	BY SIMILARITY.	DE (EPI).
FT	DISULFID	713	726	BY SIMILARITY.	DE (EPI).
FT	DISULFID	720	735	BY SIMILARITY.	DE (EPI).
FT	DISULFID	742	754	BY SIMILARITY.	DE (EPI).
FT	DISULFID	785	818	BY SIMILARITY.	DE (EPI).
FT	DISULFID	812	827	BY SIMILARITY.	DE (EPI).
FT	DISULFID	833	845	BY SIMILARITY.	DE (EPI).
FT	DISULFID	899	906	BY SIMILARITY.	DE (EPI).
FT	DISULFID	906	921	BY SIMILARITY.	DE (EPI).
FT	DISULFID	923	936	BY SIMILARITY.	DE (EPI).
FT	DISULFID	942	954	BY SIMILARITY.	DE (EPI).
FT	DISULFID	950	963	BY SIMILARITY.	DE (EPI).
FT	DISULFID	965	978	BY SIMILARITY.	DE (EPI).
FT	DISULFID	984	993	BY SIMILARITY.	DE (EPI).
FT	DISULFID	989	1002	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1004	1017	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1023	1035	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1031	1044	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1046	1060	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1066	1079	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1073	1088	BY SIMILARITY.	DE (EPI).
FT	DISULFID	1093	1105	BY SIMILARITY.	DE (EPI).
FT	CARBONYD	179	179	N-LINKED (GLCNAC. .) (POTENTIAL).	DE (EPI).
FT	CARBONYD	497	497	N-LINKED (GLCNAC. .) (POTENTIAL).	DE (EPI).
FT	CARBONYD	737	737	N-LINKED (GLCNAC. .) (POTENTIAL).	DE (EPI).
FT	CARBONYD	1072	1072	MISSING (IN ISOFORM EGF-LESS).	DE (EPI).
FT	VARSPUC	709	755	HSGRKYAAQHTVHSSCRAC -> TVA(SICWPRPRL)P	DE (EPI).
FT	CONFLICT	140	159	GF (IN REF. 2).	DE (EPI).
FT	CONFLICT	348	348	S -> L (IN REF. 2).	DE (EPI).
FT	CONFLICT	507	507	Q -> QQ (IN REF. 2).	DE (EPI).
FT	CONFLICT	1102	1102	Q -> E (IN REF. 2).	DE (EPI).
SQ	SEQUENCE	1221 AA;	131818 MW;	87DB2A10R8FDC45F CRC64;	DE (EPI).
Query Match Best Local Similarity 50.0%; Matches 9; Conservative					
Score 49.5%; Pred. No. 19; 4; Mismatches 2; Indels 3; Gaps 1;					
Length 1221; Signal 1.; 24 Tissue Factor Pathway Inhibitor.					
FT SIGNAL 1 Tissue Factor Pathway Inhibitor.					
Qy	1	DSEDEDEHTITDTELP 18	FT CHAIN 25 300 BTP1/KUNITZ INHIBITOR 1	FT DOMAIN 50 100 (VII(A))TISSUE FACTOR BINDING SITE).	FT DOMAIN 121 171 BTP1/KUNITZ INHIBITOR 2
Dy	274	DEEEEEETLVE---FP 298	FT DOMAIN 121 171 (FACTOR X(A) BINDING SITE).		

"Paradoxical transcriptional activation of rat liver cytochrome P-450 3A1 by dexamethasone and the antiglucocorticoid pregnenolone 16 alpha-carbonitrile: analysis by transient transfection into primary monolayer cultures of adult rat hepatocytes." *Proc. Natl. Acad. Sci. U.S.A.* 89:2145-2149 (1992).

-1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. IN LIVER MICROSONES, THIS ENZYME IS INVOLVED IN AN NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.

-1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.

-1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

-1- INDUCTION: BY PREGNENOLONE 16-ALPHA-CARBONITRILE (PNCN).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M10161; AAA4105.1; .
DR PROSITE; PRO00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum; Polymorphism.
FT BINDING 443 443 HEME.
FT VARIANT 207 207 T -> A (IN STRAIN WISTAR).
FT VARIANT 213 213 F -> I (IN STRAIN WISTAR).
FT VARIANT 232 232 I -> V (IN STRAIN WISTAR).
SQ SEQUENCE 504 AA; 57917 MW; CPDSAC8C37E9CADB CRC64;

Query Match 45.8%; Score 44; DB 1; Length 504;
Best Local Similarity 43.8%; Pred. No. 24; Indels 0; Gaps 0;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSEEDBEHTITDTE 16
Db 281 DSKDKESHTALSDMEI 296

RESULT 10
TRAIL_MOUSE STANDARD; PRT; 706 AA.
AC Q9CQH1; 002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (TUMOR necrosis factor type 1 receptor associated protein) (TRAP-1) (TNFR-associated protein 1).
DE Associated protein 1.

GN TRAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus. NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryonic stem cells, and Kidney;
RC MEDLINE=21085666; PubMed=11217651;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Asai J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batzalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G., Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gatinel S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlioni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch R.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilkinson L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection." *Nature* 409:685-690 (2001).
-1- FUNCTION: Chaperone that expresses an ATPase activity.(By similarity).
-1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/> or send an email to license@isb-sib.ch).
CC EMBL; AK010341; BAB26565.1; .
CC EMBL; AK002409; BAB22078.1; .
CC HSSP; P07900; 1VER.
CC MGD; MG1:1915265; Trap1.
CC InterPro; IPR003594; HATPase_C.
CC InterPro; IPR00104; HSP90.
CC Pfam; PF02518; HATPase_C; 1.
CC Pfam; PF00183; HSP90; 3.
CC PRINTS; PRO00725; HEATSHOCK90.
CC SMART; SM00387; HATPase_C; 1.
CC PROSITE; PS00298; HSP0; FALSE; NEG.
CC Chaperone; ATP-binding; Mitochondrion; Transit peptide.
KW TRANSIT 1 ?
FT CHAIN ?
FT SEQUENCE 706 AA; 80208 MW; 7183CE338CB36464 CRC64;

Query Match 45.8%; Score 44; DB 1; Length 706;
Best Local Similarity 53.3%; Pred. No. 35; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSEEDBEHTITDTE 15
Db 67 DKEEEHSHTISSTE 81

RESULT 11
M3KC_MOUSE STANDARD; PRT; 888 AA.
AC M3KC_MOUSE STANDARD; P70286; 0601700; P70286; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37) (Leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing kinase) (DLK).
DE MAPK12 OR ZPK.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus. NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.

FT	CONFFLICT	494	495	EQ -> DE (IN REF. 2).
FT	CONFLICT	517	517	N -> D (IN REF. 2).
FT	CONFLICT	794	794	E -> G (IN REF. 2).
FT	SEQUENCE	888 AA:	96083 MW:	CFECF1D34F889ABB CRC64;
RN	SEQUENCE FROM N.A.			
RP	STRAIN=ICR/Swiss Webster; TISSUE=Brain;			
RC				
RX	PHOSPHORYLATION OF MAP3K12, AND MOTAGENESIS OF LYS-185 AND GLU-192.			
RX	[3] MEDLINE=95074107; PubMed=8769565;			
RA	Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;			
RA	Matz M., Merritt S.E., Pan G.G., Holzman L.B.;			
RT	Characterization of dual leucine zipper-bearing kinase, a mixed			
RT	lineage kinase present in synaptic terminals whose phosphorylation			
RT	state is regulated by membrane depolarization via calcineurin.;			
RL	J. Biol. Chem. 271:16888-16896(1996).			
RL	-I- FUNCTION: May be an activator of the JNK/SAPK pathway.			
RL	Phosphorylates beta-casein, histone 1 and myelin basic protein in			
RL	vitro.			
RN	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
RN	-I- COFACTOR: Magnesium.			
RN	-I- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.			
CC	-I- TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart,			
CC	testis, gastrointestinal tract, stomach, liver and pancreas.			
CC	Within the nervous system, predominantly expressed in neurons and			
CC	enriched in synaptic terminals.			
CC	-I- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol			
CC	under basal conditions and dephosphorylated when membrane-			
CC	-I- ASSOCIATED: MAP KINASE KINASE SUBFAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sb-sib.ch).			
CC	-----			
CC	DR EMBL: U14636; AAA57280.1; .			
CC	DR DR: P06213; IIRK.			
CC	DR HESF; P06213; IIRK.			
CC	DR MGD; MGI:1346811; Map3k12.			
CC	DR InterPro: IPR000719; Euk_pk kinase.			
CC	DR InterPro: IPR04040; STY_pk kinase.			
CC	DR InterPro: IPR02290; Ser-thr_pk kinase.			
CC	DR SMART: SM00221; STYK; 1.			
CC	DR PFAM: PF0069; pk kinase; 1.			
CC	DR SMART: SM00221; STYK; 1.			
CC	DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
CC	DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
CC	KW Transfase; Serine/threonine-Protein kinase; ATP-binding;			
CC	KW Phosphorylation; Magnesium; Membrane.			
CC	DOMAIN 158 399 PROTEIN KINASE.			
CC	NP_BIND 164 172 ATP (BY SIMILARITY).			
CC	FT BINDING 185 185 ATP.			
CC	FT ACT_SITE 269 269 BY SIMILARITY.			
CC	FT DOMAIN 56 62 POLY-GLY.			
CC	FT DOMAIN 668 671 POLY-PRO.			
CC	FT DOMAIN 698 701 POLY-PRO.			
CC	FT DOMAIN 753 758 POLY-GLU.			
CC	FT BINDING 185 185 K->A: NO CATALYTIC ACTIVITY.			
CC	FT ACT_SITE 192 192 E->A: NO CHANGE.			
CC	FT DOMAIN 18 18 V -> A (IN REF. 2).			
CC	FT CONFLICT 28 29 KL -> NV (IN REF. 2).			
CC	FT CONFLICT 382 382 S -> T (IN REF. 2).			

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*"; *Science* 287:2185-2195(2000).

-1- FUNCTION: REGULATOR OF CELL FATE DECISIONS IN MULTIPLE LINEAGES. SPECIFICALLY, FUNCTIONS AS A PRECURSOR CELLS. PROBABLY ALSO INVOLVED IN CELL TYPE SPECIFICATION OF MALPIGHIAN TUBULES. IN ABSENCE OF CUT GENE EXTERNAL SENSORY ORGANS ARE TRANSFORMED INTO CHORDOTONAL ORGANS.

-1- SUBCELLULAR LOCATION: Nuclear (Probable).

-1- TISSUE SPECIFICITY: DETECTED IN MANY CELLS IN THE CENTRAL NERVOUS SYSTEM, ALL EXTERNAL SENSORY ORGANS, SOME PERIPHERAL NEURONS, AND IN THE NON-NEURAL CELLS OF THE SPIRACLES AND THE MALPIGHIAN TUBULES.

-1- DEVELOPMENTAL STAGE: CELL-SPECIFIC PATTERN OF EXPRESSION. BROADLY EXPRESSED DURING EMBRYONIC DEVELOPMENT.

-1- DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND HETERO-DIMERIZATION.

-1- SIMILARITY: CONTAINS 3 CUT DOMAINS.

-1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce> or send an email to license@isb-sib.ch).

DR X07985; CAA30794.1; EMBL: AE003441; AAF46264.2; .

DR PR: S03170; S03170.

DR HSSP: P04002; 1WFA.

DR TRANSFAC: T02004; .

DR FlyBase: FBgn004198; ct.

DR InterPro: IPR003350; Cut.

DR InterPro: IPR00047; BTH repressor.

DR InterPro: IPR01556; Homeobox.

DR PRAM: PF02376; cut; 3.

DR PRAM: PF00046; homeobox; 1.

DR PRINTS: PRO0031; HTHREPRESSR.

DR SMART: SM00389; HOX; 1.

DR PROSITE: PS00027; HOMEOBOX_1; 1.

DR PROSITE; PS50071; HOMEOBOX_2; 1.

KW Transcription regulation; Homeobox; DNA-binding; Homeobox; Nuclear protein; Repeat; Coiled coil.

KW Developmental Protein; Nuclear protein; Coiled coil (POTENTIAL).

FT DOMAIN 433 499 CUT 1.

FT DOMAIN 265 343 COILED COIL (POTENTIAL).

FT DOMAIN 798 964 COILED COIL (POTENTIAL).

FT DOMAIN 1056 1161 CUT 2.

FT DOMAIN 1329 1417 COILED COIL (POTENTIAL).

FT DOMAIN 1463 1522 CUT 3.

FT DOMAIN 1608 1695 HOMEOBOX.

FT DOMAIN 1745 1804 ALA/GLN-RICH.

FT DOMAIN 194 210 ALA-RICH.

FT DOMAIN 235 243 HIS/GLN-RICH (OPA-REPEAT).

FT DOMAIN 271 293 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 384 428 ASN-RICH.

FT DOMAIN 547 554 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 574 584 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 616 630 ALA-RICH.

FT DOMAIN 665 694 ALA-RICH.

FT DOMAIN 2004 2014 HIS/GLN-RICH (OPA-REPEAT).

FT DOMAIN 2071 2077 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 2124 2136 ALA/PRO-RICH.

SO SPONCE 213628 MW. 00BERNCA1600AR C864.

Query Match 45.8%; Score 44; DB 1; Length 2175;

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>)
 CC or send an e-mail to license@isb-sib.ch).

DR EMBL; J03143; AAAS2731.1;
 DR EMBL; AL050337; CAB53062.1; -;
 DR PIR; A31555; A31555;
 DR PDB; 1JTH; 25-MAR-98;
 DR PDB; 1RFG9; 11-MIG-00;
 DR GLYCOSITEDB; P15460; -;
 DR NCM; 107470; -;
 DR MIM; 209950; -;
 DR InterPro; IPR000282; Cytok-receptor-2;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
 KW Immunoglobulin domain; 3D-structure.

FT SIGNAL; 1 17
 FT CHAIN; 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN,
 FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 266 POTENTIAL.
 FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 77 85
 FT DISULFID 122 167
 FT DISULFID 195 200
 FT DISULFID 214 235
 FT CARBOYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 489 AA; 54404 MW; DCF9E574DBF47400 CRC64;

Query Match 44.8%; Score 43; DB 1; Length 489;
 Best Local Similarity 44.4%; Pred. No. 33;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 DSEDEDEHTITDTLEPP 18
 Db 415 DSCLSHSSLSSEFPP 432

Search completed: September 20, 2002, 10:32:02
 Job time: 235 sec

Qy	1	DSEDEDEHTITDTTELPP	18	RX	MEDLINE-99373128; PubMed-10441475;
		AC 045881;	PRELIMINARY;	RA	Yamada K., Printz R.L., Osawa H., Granner D.K.;
		AC 045881;	PRT: 2225 AA.	RT	*Human ZHX1: cloning, chromosomal location, and interaction with transcription factor NF-Y.;
Db	29	DSEDEDEHTITDTTELPP	46	RL	Biochem. Biophys. Res. Commun. 261:614-621(1999).
RESULT	2			RN	[2]
				RP	SEQUENCE FROM N.A.
				RA	Muellicher R., Ziegler B.L.;
				RT	*Identification and cloning of the human ZHX1 gene.;
				RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
				DR	EMBL; AF195766; AAD-0624.1;
				DR	TRANSFAC; T04355; -.
				DR	InterPro; IPR001356; Homeobox.
				DR	InterPro; IPR000822; Znf-C2H2.
				DR	Pfam; PF00046; homeobox; 4.
				DR	Pfam; PF00096; f-C2H2; 2.
				DR	SMART; SM00389; HOX; 5.
				DR	PROSITE; PS00355; Znf-C2H2; 2.
				DR	PROSITE; PS5001; HOMEobox_2; 4.
				DR	PROSITE; PS50157; ZINC_FINGER_C2H2-2; 1.
				KW	DNA-binding; Homeobox; Nuclear protein; Zinc-finger.
				SQ	SEQUENCE 873 AA; 98097 MW; 66CF1CEC5EF824E5 CRC64;
Qy	2			Query Match	53.1%
				Best Local Similarity	61.1%
				Matches	11; Conservative 1; Mismatches 1;
				6	Indels 0; Gaps 0;
				Qy	1 DSEDEDEHTITDTTELPP 18
				Db	844 DQEDEEEEDDDSDTWEPP 861
RESULT	4			P70121	PRELIMINARY; PRT; 873 AA.
				ID	P70121.
				AC	P70121-1997 (TREMBLrel. 02, Created)
				DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)
				DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
				DE	DNA-BINDING PROTEIN.
				GN	ZHX1.
				OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
				OC	NCBI_TaxID=10090;
				RN	[1]
				RP	SEQUENCE FROM N.A.
				RA	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
				DR	EMBL; Z54200; CAR99905.1;
				DR	TRANSFAC; T04356; -.
				DR	MGD; MG1:109271; zhx1.
				DR	InterPro; IPR001356; Homeobox.
				DR	InterPro; IPR000822; Znf-C2H2.
				DR	Pfam; PF00046; homeobox; 4.
				DR	Pfam; PF00096; f-C2H2; 2.
				DR	SMART; SM00389; HOX; 5.
				DR	PROSITE; PS00355; Znf-C2H2; 2.
				DR	PROSITE; PS50071; HOMEBOX_2; 4.
				DR	PROSITE; PS50157; ZINC_FINGER_C2H2-2; 1.
				KW	DNA-binding; Zinc-finger.
				SQ	SEQUENCE 873 AA; 97621 MW; 831CDE694ADCFE4F CRC64;
Qy	3			RESULT	3
				Q9UYK1	PRELIMINARY; PRT; 873 AA.
				ID	Q9UYK1.
				AC	Q9UYK1.
				DT	01-MAY-2000 (TREMBLrel. 13, Created)
				DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
				DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
				DE	ZINC FINGER HOMEobox PROTEIN ZHX1 (ZHX1 PROTEIN).
				GN	ZHX1.
				OS	'Homo sapiens' (Human).
				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
				OC	NCBI_TaxID=9666;
				RN	[1]
				RP	SEQUENCE FROM N.A.
				RC	TISSUE-LIVER;

Query Match 53.1%; Score 51; DB 11; Length 873;
 Best Local Similarity 61.1%; Pred. No. 7.4;
 Matches 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 5
 ID 00319 PRELIMINARY; PRT; 224 AA.
 AC 00319;
 DT 01-JUL-1997 (TREMBLel. 04, Created)
 DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)
 DE WW3 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-971313427; PubMed-9169421;
 RA Pirozzi G., McConnell S.J., Uveges A.J., Carter J.M., Sparks A.B.,
 RA Kay B.K., Fowlkes D.M.;
 RT "Identification of novel human WW domain-containing proteins by
 cloning of ligand targets";
 RL J. Biol. Chem. 272:14611-14616(1997).
 DR EMBL: U96115; AAC51326.1; -.
 DR InterPro; IPR00619; Guanylate_kin.
 DR InterPro; IPR00162; WW.
 DR InterPro; IPR002349; WW_domain.
 DR Pfam; PF00397; PDZ; 2.
 DR PR0397; WW; 2.
 DR PR0397; WW_DOMAIN.
 DR SMART; SM00012; Guic; 1.
 DR SMART; SM00228; PDZ; 2.
 DR SMART; SM00455; WW; 2.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 2.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS50020; WW_DOMAIN_2; 2.
 DR Kinase.
 FT NON_TER 1 1
 FT NON_TER 677 677
 SQ SEQUENCE 677 AA: 74507 MW: 984C9EB4C499D047 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 677;
 Best Local Similarity 61.1%; Pred. No. 2.1; Matches 11; Mismatches 2; Indels 4; Gaps 1;

RESULT 6
 ID 043863 PRELIMINARY; PRT; 1160 AA.
 AC 043863;
 DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)
 DT 01-JUN-1998 (TREMBLel. 06, Created)
 DE MEMBRANE ASSOCIATED GUANYLATE KINASE 1 (FRAGMENT).
 GN MAGI-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9736949; PubMed-9225980;
 RA Marcollis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kigwai A.S.,
 RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;

RESULT 7
 ID 096028 PRELIMINARY; PRT; 1160 AA.
 AC 096028;
 DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLel. 19, Last annotation update)
 DE MAGI-1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laura R.P., Lasky L.A.;
 RT "MAGI-1: a widely expressed, alternatively spliced tight junction
 protein";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041655; AAC40651; -.
 SQ SEQUENCE 1160 AA: 126558 MW: 788E5B621AC295B0 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 1160;
 Best Local Similarity 61.1%; Pred. No. 1.2; Matches 11; Mismatches 2; Indels 1; Gaps 1;

RESULT 8
 ID 075085 PRELIMINARY; PRT; 1160 AA.
 AC 075085;
 DT 01-DEC-2001 (TREMBLel. 19, Last annotation update)
 DE MEMBRANE ASSOCIATED GUANYLATE KINASE 1 (FRAGMENT).
 GN MAGI-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9736949; PubMed-9225980;
 RA Marcollis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kigwai A.S.,
 RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;

RT "CDNA with long CAG trinucleotide repeats from human brain.";
 RL Hum. Genet. 100:114-122(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98311405; PubMed-9647693;
 RA Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K.; Kushl J.,
 Kaminsky Z., Kleiderlein J.J., Sharp A.H., Ross C.A.;
 RT "Atrophin-1, the DPLA gene product, interacts with two families of WW
 domain-containing proteins.";
 RL Mol. Cell. Neurosci. 11:149-160(1998).
 DR EMBL: UB0754; AAC08441; -.
 DR InterPro; IPR00619; Guanylate_kin.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW.
 DR InterPro; IPR002349; WW_domain.
 DR Pfam; PF00595; PDZ; 2.
 DR Pfam; PF00397; WW; 2.
 DR PR0397; WW; 2.
 DR PR0397; WW_DOMAIN.
 DR SMART; SM00012; Guic; 1.
 DR SMART; SM00228; PDZ; 2.
 DR SMART; SM00455; WW; 2.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 2.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS50020; WW_DOMAIN_2; 2.
 DR Kinase.
 FT NON_TER 1 1
 FT NON_TER 677 677
 SQ SEQUENCE 677 AA: 74507 MW: 984C9EB4C499D047 CRC64;

ID	PRELIMINARY;	PRT;	1256 AA.	Matches	11;	Conservative	2;	Mismatches	4;	Indels	1;	Gaps	1;
AC	075085;			QY	1	DSEEDBEHTITDTEIPP	18						
DT	01-NOV-1998; *TREMBLrel. 08, Created			AC	1	1	1	1	1	1	1		
DT	01-NOV-1998; *TREMBLrel. 08, Last sequence update			DB	254	DSGEDEHTT-LQETALPP	270						
DE	BAI1-ASSOCIATED PROTEIN 1.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RC	TISSUE-BRAIN;												
RD	MEDLINE-98321173; PubMed=9647739;												
RX	Shirahiro T., Futamura M., Oda K., Nishimori H., Nakamura Y., Tokino T.												
RA													
RT	"Cleaving and characterization of BAI1-associated protein 1: a PDZ domain-containing protein that interacts with BAI1." Biochem. Biophys. Res. Commun. 247:597-604(1998).												
RT	InterPro: IPR006119; Guanylate_kin.												
DR	InterPro: IPR001478; PDZ.												
DR	InterPro: IPR001202; WW.												
DR	InterPro: IPR001349; WW_domain.												
DR	EMBL: P31016; 1BE9												
DR	PFAM: PF00525; Guanylate_kin.												
DR	PFAM: PF00595; PDZ.												
DR	PFAM: PF003597; WW.												
DR	SMART: SMART0072; GuRK1.												
DR	SMART: SMART0228; PDZ.												
DR	SMART: SMART0456; WW.												
DR	PROSITE: PS000856; GUANYLATE_KINASE_1.												
DR	PROSITE: PS00052; GUANYLATE_KINASE_2;												
DR	PROSITE: PS01106; PDZ.												
DR	PROSITE: PS01159; WW_DOMAIN_1.												
DR	PROSITE: PS00020; WW_DOMAIN_2.												
SQ	SEQUENCE: 1256 AA; 136981 MW; 83FADE2091A4C8E4 CRC64;												
RESULT	9												
Q96QZ9	PRELIMINARY;	PRT;	1287 AA.	Query Match	52.8%	Score 50.5;	DB 4;	Length 1256;					
ID	Q96QZ9			Best Local Similarity	61.1%	Pred. No. 13;	2;	Mismatches	4;	Indels	1;	Gaps	1;
AC	096QZ9;			Matches	11;	Conservative	2;	Mismatches	4;	Indels	1;	Gaps	1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)												
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)												
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)												
DE	MAGI-1B ALPHA_BETA.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RA	Laura R.P., Lasky L.A.;												
RT	"MAGI-1: a widely expressed, alternatively spliced tight junction protein."												
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.												
DR	EMBL: AF401654; AAC94064.1;												
SQ	SEQUENCE: 1287 AA; 140439 MW; C676655657BDE0D5 CRC64;												
RESULT	12												
Q91LG7	PRELIMINARY;	PRT;	1044 AA.	Query Match	52.6%	Score 50.5;	DB 4;	Length 1287;					
ID	Q91LG7			Best Local Similarity	61.1%	Pred. No. 13;	2;	Mismatches	3;	Indels	5;	Gaps	1;
AC	091LG7;			Matches	10;	Conservative	2;	Mismatches	3;	Indels	5;	Gaps	1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)												
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)												
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)												
DE	MAGI-1B ALPHA_BETA.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RA	Laura R.P., Lasky L.A.;												
RT	"MAGI-1: a widely expressed, alternatively spliced tight junction protein."												
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.												
DR	EMBL: BC017179; AAC941719.1;												
KW	HYPOTHETICAL protein.												
FT	NON_TER												
SQ	SEQUENCE: 526 AA; 58854 MW; 555A6529B6CEB211 CRC64;												
RESULT	11												
Q96AG1	PRELIMINARY;	PRT;	526 AA.	Query Match	52.6%	Score 50.5;	DB 4;	Length 1462;					
ID	Q96AG1			Best Local Similarity	61.1%	Pred. No. 15;	2;	Mismatches	4;	Indels	1;	Gaps	1;
AC	Q96AG1;			Matches	11;	Conservative	2;	Mismatches	4;	Indels	1;	Gaps	1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)												
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)												
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)												
DE	Hypothetical protein.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RA	Strainsberg R.;												
RT	"Tissue-EYE, AND RETINOBLASTOMA;"												
RT	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.												
DR	EMBL: BC017179; AAC941719.1;												
KW	HYPOTHETICAL protein.												
FT	NON_TER												
SQ	SEQUENCE: 526 AA; 58854 MW; 555A6529B6CEB211 CRC64;												
RESULT	10												
Q96QZ7	PRELIMINARY;	PRT;	1462 AA.	Query Match	51.6%	Score 49.5;	DB 4;	Length 526;					
ID	Q96QZ7			Best Local Similarity	55.6%	Pred. No. 7.6;	3;	Mismatches	0;	Indels	5;	Gaps	1;
AC	Q96QZ7;			Matches	10;	Conservative	2;	Mismatches	3;	Indels	5;	Gaps	1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)												
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)												
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)												
DE	MAGI-1B ALPHA_BETA.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RA	Laura R.P., Lasky L.A.;												
RT	"MAGI-1: a widely expressed, alternatively spliced tight junction protein."												
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.												
DR	EMBL: AF401654; AAC94064.1;												
SQ	SEQUENCE: 1287 AA; 140439 MW; C676655657BDE0D5 CRC64;												
RESULT	12												
Q91LG7	PRELIMINARY;	PRT;	1044 AA.	Query Match	52.6%	Score 50.5;	DB 4;	Length 1287;					
ID	Q91LG7			Best Local Similarity	61.1%	Pred. No. 13;	2;	Mismatches	3;	Indels	5;	Gaps	1;
AC	Q91LG7;			Matches	10;	Conservative	2;	Mismatches	3;	Indels	5;	Gaps	1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)												
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)												
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)												
DE	MAGI-1B ALPHA_BETA.												
OS	Homo sapiens (Human)												
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
OX	NCBI_TaxID=9606;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RA	Laura R.P., Lasky L.A.;												
RT	"MAGI-1: a widely expressed, alternatively spliced tight junction protein."												
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.												
DR	EMBL: AF401654; AAC94064.1;												
SQ	SEQUENCE: 1287 AA; 140439 MW; C676655657BDE0D5												

AC 091LG7; PRELIMINARY; PRT: 1174 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE ORF73.
 OS White spot syndrome virus (WSSV).
 OC Viruses; Unassigned viruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21342572; PUBMED-11448154;
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vliak J.M.,
 RT "The white spot syndrome virus DNA genome sequence.",
 RL Virology 286:7-22(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF319029; AAK7742.1;
 DR SEQUENCE 1044 AA; 117929 MW; 9E43EC532320B3E CRC64;

Query Match 51.0%; Score 49; DB 12; Length 1044;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITDTE 15
 DB 152 DSEEESEEDIVDDE 166

RESULT 13.

ID 097806 PRELIMINARY; PRT: 585 AA.
 AC 097806;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DE FERREDOXIN OXIDOREDUCTASE.
 GN TVG1-06112.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
 OC Thermoplasma.
 OX NCBI_Taxid-50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GS1 / DSM 4299 / JCM 9571;
 RX MEDLINE-20510466; PUBMED-11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima-Ohyu Y., Watanabe K., Yamazaki M., Kanehira K., Kawamoto T.,
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium.",
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL: AP005996; BAB60501.1; -.
 DR Interpro: IPR02869; POR.
 DR Interpro: IPR02880; POR_N.
 DR Pfam: PF01558; POR; 1.
 DR Pfam: PF01855; POR_N; 1.
 KW Complete proteome.
 SO SEQUENCE 585 AA; 63978 MW; DD061R862266DFCD CRC64;

Query Match 50.0%; Score 48; DB 17; Length 585;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITDTE 18
 DB 151 DSEEESEEDIVDDE 162

RESULT 14.

ID 099K58 PRELIMINARY; PRT: 1174 AA.
 AC 099K58;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE SIMILAR TO FIBULIN 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
 RA Strauberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC005443; AAH05443.1; -.
 DR HSSP; P00736; 1AP0.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; AxS hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR Pfam; PF01821; ANATO; 2.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00181; EGF; 11.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS0116; EGF_2; 5.
 DR PROSITE; PS01187; EGF_Ca; 9.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SO SEQUENCE 1174 AA; 126460 MW; 8D628AC710FFBA6B8 CRC64;

Query Match 49.5%; Score 47.5; DB 11; Length 1174;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 DSEDEDEHTITDTE 18
 DB 274 DSEEESEEDIVDDE 288

RESULT 15.

ID 006810 PRELIMINARY; PRT: 360 AA.
 AC 006810;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHROMOSOME XVI COSMID 9513.
 GN YP9513.9 OR YP075C.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Sakkaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomyctaceae; Saccharomyces.
 OX NCBI_Taxid-4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C (AB972);
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RL couch J.;
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C (AB972);
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,

RA Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L.,
RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C (AB97:2);

RA Waterston R.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Edwards M.C., Liegeois N., Horecka J., Depinhho R.A., Sprague G.F.,

RA Tyers M., Ellledge S.J.;

RL Genetics 0,0-0(1997);

DR U516263; AAB6816.1;

DR EMBL; AF016263; AAB81506.1;

DR SGD; S006279; OPY2.

SEQUENCE 360 AA; 38901 MW; 6D44AFA25042FFB CRC64;

Query Match Similarity 49.08; Score 47; DB 3; Length 360;
Best Local Similarity 47.18; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DSEEDBEHTITDTELP 17

Db 1 :111 :1 |1|1|

318 DEDDDDEGSFIDLEIP 334

Search completed: September 20, 2002, 10:31:03
Job time: 225 sec